

WO98020157

Publication Title:

No title available

Abstract:

Abstract not available for WO98020157 Data supplied from the esp@cenet database - Worldwide

Courtesy of <http://v3.espacenet.com>



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY-(PCT)

(51) International Patent Classification ⁶ : C12Q 1/68	A2	(11) International Publication Number: WO 98/20157 (43) International Publication Date: 14 May 1998 (14.05.98)
(21) International Application Number: PCT/CA97/00829 (22) International Filing Date: 4 November 1997 (04.11.97) (30) Priority Data: 08/743,637 4 November 1996 (04.11.96) US (71) Applicant (for all designated States except US): INFECTIO DIAGNOSTIC (I.D.I.) INC. [CA/CA]; 4 ^{ème} étage, 2050, boulevard René Lévesque Ouest, Sainte-Foy, Québec G1V 2K8 (CA). (72) Inventors; and (75) Inventors/Applicants (for US only): BERGERON, Michel, G. [CA/CA]; 2069, rue Brûlard, Sillery, Québec G1T 1G2 (CA). PICARD, François, J. [CA/CA]; 1245, rue de la Sapinière, Cap-Rouge, Québec G1Y 1A1 (CA). OUELLETTE, Marc [CA/CA]; 1035 de Ploermel, Sillery, Québec G1S 3S1 (CA). ROY, Paul, H. [US/US]; 28, rue Charles Garnier, Loretteville, Québec G2A 2X8 (CA). (74) Agents: DUBUC, Jean, H. et al.; Goudreau Gage Dubuc & Martineau Walker, The Stock Exchange Tower, Suite 3400, 800 Place Victoria, P.O. Box 242, Montreal, Québec H4Z 1E9 (CA).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: SPECIES-SPECIFIC, GENUS-SPECIFIC AND UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL AND FUNGAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS FOR DIAGNOSIS IN MICROBIOLOGY LABORATORIES		
(57) Abstract DNA-based methods employing amplification primers or probes for detecting, identifying, and quantifying in a test sample DNA from (i) any bacterium, (ii) the species <i>Streptococcus agalactiae</i> , <i>Staphylococcus saprophyticus</i> , <i>Enterococcus faecium</i> , <i>Neisseria meningitidis</i> , <i>Listeria monocytogenes</i> and <i>Candida albicans</i> , and (iii) any species of the genera <i>Streptococcus</i> , <i>Staphylococcus</i> , <i>Enterococcus</i> , <i>Neisseria</i> and <i>Candida</i> are disclosed. DNA-based methods employing amplification primers or probes for detecting, identifying, and quantifying in a test sample antibiotic resistance genes selected from the group consisting of <i>bla_{tem}</i> , <i>bla_{rob}</i> , <i>bla_{shv}</i> , <i>bla_{oxa}</i> , <i>bla_Z</i> , <i>aadB</i> , <i>aacC1</i> , <i>aacC2</i> , <i>aacC3</i> , <i>aacA4</i> , <i>aac6'-IIa</i> , <i>ermA</i> , <i>ermB</i> , <i>ermC</i> , <i>mecA</i> , <i>vanA</i> , <i>vanB</i> , <i>vanC</i> , <i>satA</i> , <i>aac(6'-aph(2''))</i> , <i>aad(6')</i> , <i>vat</i> , <i>vga</i> , <i>msrA</i> , <i>sul</i> and <i>int</i> are also disclosed. The above microbial species, genera and resistance genes are all clinically relevant and commonly encountered in a variety of clinical specimens. These DNA-based assays are rapid, accurate and can be used in clinical microbiology laboratories for routine diagnosis. These novel diagnostic tools should be useful to improve the speed and accuracy of diagnosis of microbial infections, thereby allowing more effective treatments. Diagnostic kits for (i) the universal detection and quantification of bacteria, and/or (ii) the detection, identification and quantification of the above-mentioned bacterial and fungal species and/or genera, and/or (iii) the detection, identification and quantification of the above-mentioned antibiotic resistance genes are also claimed.		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece			TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	NZ	New Zealand		
CM	Cameroon			PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

TITLE OF THE INVENTION

SPECIES-SPECIFIC, GENUS-SPECIFIC AND UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL AND FUNGAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS FOR DIAGNOSIS IN MICROBIOLOGY LABORATORIES

BACKGROUND OF THE INVENTION**Classical methods for the identification and susceptibility testing of bacteria**

Bacteria are classically identified by their ability to utilize different substrates as a source of carbon and nitrogen through the use of biochemical tests such as the API20E™ system (bioMérieux). For susceptibility testing, clinical microbiology laboratories use methods including disk diffusion, agar dilution and broth microdilution. Although identifications based on biochemical tests and antibacterial susceptibility tests are cost-effective, at least two days are required to obtain preliminary results due to the necessity of two successive overnight incubations to identify the bacteria from clinical specimens as well as to determine their susceptibility to antimicrobial agents. There are some commercially available automated systems (i.e. the MicroScan system from Dade Diagnostics Corp. and the Vitek system from bioMérieux) which use sophisticated and expensive apparatus for faster microbial identification and susceptibility testing (Stager and Davis, 1992, Clin. Microbiol. Rev. 5:302-327). These systems require shorter incubation periods, thereby allowing most bacterial identifications and susceptibility testing to be performed in less than 6 hours. Nevertheless, these faster systems always require the primary isolation of the bacteria as a pure culture, a process which takes at least 18 hours for a pure culture or 2 days for a mixed culture. The fastest identification system, the autoSCAN-Walk-Away™ system (Dade Diagnostics Corp.) identifies both gram-negative and gram-positive bacterial species from standardized inoculum in as little as 2 hours and gives susceptibility patterns to most antibiotics in 5.5 hours. However, this system has a particularly high percentage (i.e. 3.3 to 40.5%) of non-conclusive identifications with bacterial species other than *Enterobacteriaceae* (Croizé J., 1995, Lett. Infectiol. 10:109-113; York *et al.*, 1992, J. Clin. Microbiol. 30:2903-2910). For *Enterobacteriaceae*, the percentage of non-conclusive identifications was 2.7 to 11.4%.

A wide variety of bacteria and fungi are routinely isolated and identified from clinical specimens in microbiology laboratories. Tables 1 and 2 give the incidence for the most commonly isolated bacterial and fungal pathogens from various types of clinical specimens. These pathogens are the most frequently associated with nosocomial and community-acquired human infections and are therefore considered the most clinically important.

Clinical specimens tested in clinical microbiology laboratories

Most clinical specimens received in clinical microbiology laboratories are urine and blood samples. At the microbiology laboratory of the Centre Hospitalier de l'Université Laval (CHUL), urine and blood account for approximately 55% and 30% of the specimens received, respectively (Table 3). The remaining 15% of clinical specimens comprise various biological fluids including sputum, pus, cerebrospinal fluid, synovial fluid, and others (Table 3). Infections of the urinary tract, the respiratory tract and the bloodstream are usually of bacterial etiology and require antimicrobial therapy. In fact, all clinical samples received in the clinical microbiology laboratory are tested routinely for the identification of bacteria and susceptibility testing.

Conventional pathogen identification from clinical specimens**Urine specimens**

The search for pathogens in urine specimens is so preponderant in the routine microbiology laboratory that a myriad of tests have been developed. However, the gold standard remains the classical semi-quantitative plate culture method in which 1 µL of urine is streaked on plates and incubated for 18-24 hours. Colonies are then counted to determine the total number of colony forming units (CFU) per liter of urine. A bacterial urinary tract infection (UTI) is normally associated with a bacterial count of 10^7 CFU/L or more in urine. However, infections with less than 10^7 CFU/L in urine are possible, particularly in patients with a high incidence of diseases or those catheterized (Stark and Maki, 1984, N. Engl. J. Med. **311**:560-564). Importantly, approximately 80% of urine specimens tested in clinical microbiology laboratories are considered negative (i.e. bacterial count of less than 10^7 CFU/L; Table 3). Urine specimens found positive by culture are further characterized using standard biochemical tests to identify the bacterial pathogen and are also tested for susceptibility to antibiotics. The biochemical and susceptibility testing normally require 18-24 hours of incubation.

Accurate and rapid urine screening methods for bacterial pathogens would allow a faster identification of negative specimens and a more efficient treatment and care management of patients. Several rapid identification methods (Uriscreen™, UTIscreen™, Flash Track™ DNA probes and others) have been compared to slower standard biochemical methods, which are based on culture of the bacterial pathogens. Although much faster, these rapid tests showed low sensitivities and poor specificities as well as a high number of false negative and false positive results (Koenig *et al.*, 1992, J. Clin. Microbiol. **30**:342-345; Pezzlo *et al.*, 1992, J. Clin. Microbiol. **30**:640-684).

Blood specimens

The blood specimens received in the microbiology laboratory are always submitted for culture. Blood culture systems may be manual, semi-automated or completely automated. The BACTEC system (from Becton Dickinson) and the

BacTAlert system (from Organon Teknika Corporation) are the two most widely used automated blood culture systems. These systems incubate blood culture bottles under optimal conditions for bacterial growth. Bacterial growth is monitored continuously to detect early positives by using highly sensitive bacterial growth detectors. Once growth is detected, a Gram stain is performed directly from the blood culture and then used to inoculate nutrient agar plates. Subsequently, bacterial identification and susceptibility testing are carried out from isolated bacterial colonies with automated systems as described previously. The bottles are normally reported as negative if no growth is detected after an incubation of 6 to 7 days. Normally, the vast majority of blood cultures are reported negative. For example, the percentage of negative blood cultures at the microbiology laboratory of the CHUL for the period February 1994-January 1995 was 93.1% (Table 3).

Other clinical samples

Upon receipt by the clinical microbiology laboratory, all body fluids other than blood and urine that are from normally sterile sites (i.e. cerebrospinal, synovial, pleural, pericardial and others) are processed for direct microscopic examination and subsequent culture. Again, most clinical samples are negative for culture (Table 3).

Regarding clinical specimens which are not from sterile sites such as sputum or stool specimens, the laboratory diagnosis by culture is more problematic because of the contamination by the normal flora. The bacterial pathogens potentially associated with the infection are purified from the contaminants and then identified as described previously. Of course, the universal detection of bacteria would not be useful for the diagnosis of bacterial infections at these non sterile sites. On the other hand, DNA-based assays for species or genus detection and identification as well as for the detection of antibiotic resistance genes from these specimens would be very useful and would offer several advantages over classical identification and susceptibility testing methods.

DNA-based assays with any clinical specimens

There is an obvious need for rapid and accurate diagnostic tests for bacterial detection and identification directly from clinical specimens. DNA-based technologies are rapid and accurate and offer a great potential to improve the diagnosis of infectious diseases (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). The DNA probes and amplification primers which are objects of the present invention are applicable for bacterial or fungal detection and identification directly from any clinical specimens such as blood cultures, blood, urine, sputum, cerebrospinal fluid, pus and other type of specimens (Table 3). The DNA-based tests proposed in this invention are superior in terms of both rapidity and accuracy to standard biochemical methods currently used for routine diagnosis from any clinical specimens in microbiology laboratories. Since

these tests are performed in around only one hour, they provide the clinicians with new diagnostic tools which should contribute to increase the efficiency of therapies with antimicrobial agents. Clinical specimens from organisms other than humans (e.g. other primates, birds, plants, mammals, farm animals, livestock and others) may also be tested with these assays.

A high percentage of culture negative specimens

Among all the clinical specimens received for routine diagnosis, approximately 80% of urine specimens and even more (around 95%) for other types of clinical specimens are negative for the presence of bacterial pathogens (Table 3). It would also be desirable, in addition to identify bacteria at the species or genus level in a given specimen, to screen out the high proportion of negative clinical specimens with a test detecting the presence of any bacterium (i.e. universal bacterial detection). Such a screening test may be based on the DNA amplification by PCR of a highly conserved genetic target found in all bacteria. Specimens negative for bacteria would not be amplified by this assay. On the other hand, those that are positive for bacteria would give a positive amplification signal with this assay.

Towards the development of rapid DNA-based diagnostic tests

A rapid diagnostic test should have a significant impact on the management of infections. DNA probe and DNA amplification technologies offer several advantages over conventional methods for the identification of pathogens and antibiotic resistance genes from clinical samples (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.; Ehrlich and Greenberg, 1994, PCR-based Diagnostics in Infectious Disease, Blackwell Scientific Publications, Boston, MA). There is no need for culture of the bacterial pathogens, hence the organisms can be detected directly from clinical samples, thereby reducing the time associated with the isolation and identification of pathogens. Furthermore, DNA-based assays are more accurate for bacterial identification than currently used phenotypic identification systems which are based on biochemical tests. Commercially available DNA-based technologies are currently used in clinical microbiology laboratories, mainly for the detection and identification of fastidious bacterial pathogens such as *Mycobacterium tuberculosis*, *Chlamydia trachomatis*, *Neisseria gonorrhoeae* as well as for the detection of a variety of viruses (Podzorski and Persing, Molecular detection and identification of microorganisms, *In* : P. Murray *et al.*, 1995, Manual of Clinical Microbiology, ASM press, Washington D.C.). There are also other commercially available DNA-based assays which are used for culture confirmation assays.

Others have developed DNA-based tests for the detection and identification of bacterial pathogens which are objects of the present invention: *Staphylococcus* spp. (US patent application serial No. US 5 437 978), *Neisseria* spp. (US patent application

serial No. US 5 162 199 and European patent application serial No. EP 0 337 896 131) and *Listeria monocytogenes* (US patent applications serial Nos US 5 389 513 and US 5 089 386). However, the diagnostic tests described in these patents are based either on rRNA genes or on genetic targets different from those described in the present invention.

Although there are diagnostic kits or methods already used in clinical microbiology laboratories, there is still a need for an advantageous alternative to the conventional culture identification methods in order to improve the accuracy and the speed of the diagnosis of commonly encountered bacterial infections. Besides being much faster, DNA-based diagnostic tests are more accurate than standard biochemical tests presently used for diagnosis because the bacterial genotype (e.g. DNA level) is more stable than the bacterial phenotype (e.g. metabolic level).

Knowledge of the genomic sequences of bacterial and fungal species continuously increases as testified by the number of sequences available from databases. From the sequences readily available from databases, there is no indication therefrom as to their potential for diagnostic purposes. For determining good candidates for diagnostic purposes, one could select sequences for DNA-based assays for (i) the species-specific detection and identification of commonly encountered bacterial or fungal pathogens, (ii) the genus-specific detection and identification of commonly encountered bacterial or fungal pathogens, (iii) the universal detection of bacterial or fungal pathogens and/or (iv) the specific detection and identification of antibiotic resistance genes. All of the above types of DNA-based assays may be performed directly from any type of clinical specimens or from a microbial culture.

In our co-pending U.S. (N.S. 08/526,840) and PCT (PCT/CA/95/00528) patent applications, we described DNA sequences suitable for (i) the species-specific detection and identification of 12 clinically important bacterial pathogens, (ii) the universal detection of bacteria, and (iii) the detection of 17 antibiotic resistance genes. This co-pending application described proprietary DNA sequences and DNA sequences selected from databases (in both cases, fragments of at least 100 base pairs), as well as oligonucleotide probes and amplification primers derived from these sequences. All the nucleic acid sequences described in this patent application enter the composition of diagnostic kits and methods capable of a) detecting the presence of bacteria, b) detecting specifically the presence of 12 bacterial species and 17 antibiotic resistance genes. However, these methods and kits need to be improved, since the ideal kit and method should be capable of diagnosing close to 100% of microbial pathogens and antibiotic resistance genes. For example, infections caused by *Enterococcus faecium* have become a clinical problem because of its resistance to many antibiotics. Both the detection of these bacteria and the evaluation of their

resistance profiles are desirable. Besides that, novel DNA sequences (probes and primers) capable of recognizing the same and other microbial pathogens or the same and additional antibiotic resistance genes are also desirable to aim at detecting more target genes and complement our earlier patent application.

5

STATEMENT OF THE INVENTION

It is an object of the present invention to provide a specific, ubiquitous and sensitive method using probes and/or amplification primers for determining the presence and/or amount of nucleic acids:

10 - from specific microbial species or genera selected from the group consisting of *Streptococcus* species, *Streptococcus agalactiae*, *Staphylococcus* species, *Staphylococcus saprophyticus*, *Enterococcus* species, *Enterococcus faecium*, *Neisseria* species, *Neisseria meningitidis*, *Listeria monocytogenes*, *Candida* species and *Candida albicans*

15 - from an antibiotic resistance gene selected from the group consisting of *bla_{tem}*, *bla_{rob}*, *bla_{shv}*, *bla_{oxa}*, *blaZ*, *aadB*, *aacC1*, *aacC2*, *aacC3*, *aacA4*, *aac6'-IIa*, *ermA*, *ermB*, *ermC*, *mecA*, *vanA*, *vanB*, *vanC*, *satA*, *aac(6')-aph(2'')*, *aad(6')*, *vat*, *vga*, *msrA*, *sul* and *int*, and optionally,

 - from any bacterial species

20 in any sample suspected of containing said nucleic acids,

 wherein each of said nucleic acids or a variant or part thereof comprises a selected target region hybridizable with said probe or primers;

 said method comprising the steps of contacting said sample with said probes or primers and detecting the presence and/or amount of hybridized probes or amplified products as an indication of the presence and/or amount of said any bacterial species, 25 specific microbial species or genus and antibiotic resistance gene.

 In a specific embodiment, a similar method directed to each specific microbial species or genus detection and identification, antibiotic resistance genes detection, and universal bacterial detection, separately, is provided.

30 In a more specific embodiment, the method makes use of DNA fragments (proprietary fragments and fragments obtained from databases), selected for their capacity to sensitively, specifically and ubiquitously detect the targeted bacterial or fungal nucleic acids.

 In a particularly preferred embodiment, oligonucleotides of at least 12 nucleotides in length have been derived from the longer DNA fragments, and are used 35 in the present method as probes or amplification primers.

 The proprietary oligonucleotides (probes and primers) are also another object of the invention.

 Diagnostic kits comprising probes or amplification primers for the detection of

a microbial species or genus selected from the group consisting of *Streptococcus* species, *Streptococcus agalactiae*, *Staphylococcus* species, *Staphylococcus saprophyticus*, *Enterococcus* species, *Enterococcus faecium*, *Neisseria* species, *Neisseria meningitidis*, *Listeria monocytogenes*, *Candida* species and *Candida albicans* are also objects of the present invention.

Diagnostic kits further comprising probes or amplification primers for the detection of an antibiotic resistance gene selected from the group consisting of *bla_{tem}*, *bla_{rob}*, *bla_{shv}*, *bla_{oxa}*, *blaZ*, *aadB*, *aacC1*, *aacC2*, *aacC3*, *aacA4*, *aac6'-IIa*, *ermA*, *ermB*, *ermC*, *mecA*, *vanA*, *vanB*, *vanC*, *satA*, *aac(6')-aph(2'')*, *aad(6')*, *vat*, *vga*, *msrA*, *sul* and *int* are also objects of this invention.

Diagnostic kits further comprising probes or amplification primers for the detection of any bacterial or fungal species, comprising or not comprising those for the detection of the specific microbial species or genus listed above, and further comprising or not comprising probes and primers for the antibiotic resistance genes listed above, are also objects of this invention.

In a preferred embodiment, such a kit allows for the separate or the simultaneous detection and identification of the above-listed microbial species or genus, antibiotic resistance genes and for the detection of any bacterium.

In the above methods and kits, amplification reactions may include a) polymerase chain reaction (PCR), b) ligase chain reaction, c) nucleic acid sequence-based amplification, d) self-sustained sequence replication, e) strand displacement amplification, f) branched DNA signal amplification, g) transcription-mediated amplification, h) cycling probe technology (CPT) i) nested PCR, or j) multiplex PCR.

In a preferred embodiment, a PCR protocol is used as an amplification reaction.

In a particularly preferred embodiment, a PCR protocol is provided, comprising, for each amplification cycle, an annealing step of 30 seconds at 45-55°C and a denaturation step of only one second at 95°C, without any time allowed specifically for the elongation step. This PCR protocol has been standardized to be suitable for PCR reactions with all selected primer pairs, which greatly facilitates the testing because each clinical sample can be tested with universal, species-specific, genus-specific and antibiotic resistance gene PCR primers under uniform cycling conditions. Furthermore, various combinations of primer pairs may be used in multiplex PCR assays.

We aim at developing a rapid test or kit to discard rapidly all the samples which are negative for bacterial cells and to subsequently detect and identify the above bacterial and/or fungal species and genera and to determine rapidly the bacterial resistance to antibiotics. Although the sequences from the selected antibiotic resistance genes are available from databases and have been used to develop DNA-based tests for their detection, our approach is unique because it represents a major improvement over current gold standard diagnostic methods based on bacterial

cultures. Using an amplification method for the simultaneous bacterial detection and identification and antibiotic resistance genes detection, there is no need for culturing the clinical sample prior to testing. Moreover, a modified PCR protocol has been developed to detect all target DNA sequences in approximately one hour under uniform amplification conditions. This procedure will save lives by optimizing treatment, will diminish antibiotic resistance because less antibiotics will be prescribed, will reduce the use of broad spectrum antibiotics which are expensive, decrease overall health care costs by preventing or shortening hospitalizations, and decrease the time and costs associated with clinical laboratory testing.

In the methods and kits described herein below, the oligonucleotide probes and amplification primers have been derived from larger sequences (i.e. DNA fragments of at least 100 base pairs). All DNA fragments have been obtained either from proprietary fragments or from databases. DNA fragments selected from databases are newly used in a method of detection according to the present invention, since they have been selected for their diagnostic potential.

It is clear to the individual skilled in the art that other oligonucleotide sequences appropriate for (i) the universal bacterial detection, (ii) the detection and identification of the above microbial species or genus and (iii) the detection of antibiotic resistance genes other than those listed in Annex VI may also be derived from the proprietary fragments or selected database sequences. For example, the oligonucleotide primers or probes may be shorter or longer than the ones we have chosen; they may also be selected anywhere else in the proprietary DNA fragments or in the sequences selected from databases; they may be also variants of the same oligonucleotide. If the target DNA or a variant thereof hybridizes to a given oligonucleotide, or if the target DNA or a variant thereof can be amplified by a given oligonucleotide PCR primer pair, the converse is also true; a given target DNA may hybridize to a variant oligonucleotide probe or be amplified by a variant oligonucleotide PCR primer. Alternatively, the oligonucleotides may be designed from any DNA fragment sequences for use in amplification methods other than PCR. Consequently, the core of this invention is the identification of universal, species-specific, genus-specific and resistance gene-specific genomic or non-genomic DNA fragments which are used as a source of specific and ubiquitous oligonucleotide probes and/or amplification primers. Although the selection and evaluation of oligonucleotides suitable for diagnostic purposes requires much effort, it is quite possible for the individual skilled in the art to derive, from the selected DNA fragments, oligonucleotides other than the ones listed in Annex VI which are suitable for diagnostic purposes. When a proprietary fragment or a database sequence is selected for its specificity and ubiquity, it increases the probability that subsets thereof will also be specific and ubiquitous.

Since a high percentage of clinical specimens are negative for bacteria (Table

3), DNA fragments having a high potential for the selection of universal oligonucleotide probes or primers were selected from proprietary and database sequences. The amplification primers were selected from a gene highly conserved in bacteria and fungi, and are used to detect the presence of any bacterial pathogen in clinical specimens in order to determine rapidly (approximately one hour) whether it is positive or negative for bacteria. The selected gene, designated *tuf*, encodes a protein (EF-Tu) involved in the translational process during protein synthesis. The *tuf* gene sequence alignments used to derive the universal primers include both proprietary and database sequences (Example 1 and Annex I). This strategy allows the rapid screening of the numerous negative clinical specimens (around 80% of the specimens received, see Table 3) submitted for bacteriological testing. Tables 4, 5 and 6 provide a list of the bacterial or fungal species used to test the specificity of PCR primers and DNA probes. Table 7 gives a brief description of each species-specific, genus-specific and universal amplification assays which are objects of the present invention. Tables 8, 9 and 10 provide some relevant information about the proprietary and database sequences selected for diagnostic puposes.

DETAILED DESCRIPTION OF THE INVENTION

Development of species-specific, genus-specific, universal and antibiotic resistance gene-specific DNA probes and amplification primers for microorganisms

Selection from databases of sequences suitable for diagnostic purposes

In order to select sequences which are suitable for species-specific or genus-specific detection and identification of bacteria or fungi or, alternatively, for the universal detection of bacteria, the database sequences (GenBank, EMBL and Swiss-Prot) were chosen based on their potential for diagnostic purposes according to sequence information and computer analysis performed with these sequences. Initially, all sequence data available for the targeted microbial species or genus were carefully analyzed. The gene sequences which appeared the most promising for diagnostic purposes based on sequence information and on sequence comparisons with the corresponding gene in other microbial species or genera performed with the Genetics Computer Group (GCG, Wisconsin) programs were selected for testing by PCR. Optimal PCR amplification primers were chosen from the selected database sequences with the help of the Oligo™ 4.0 primer analysis software (National Biosciences Inc., Plymouth, Minn.). The chosen primers were tested in PCR assays for their specificity and ubiquity for the target microbial species or genus. In general, the identification of database sequences from which amplification primers suitable for species-specific or genus-specific detection and identification were selected involved the computer analysis and PCR testing of several candidate gene sequences before

obtaining a primer pair which is specific and ubiquitous for the target microbial species or genus. Annex VI provides a list of selected specific and ubiquitous PCR primer pairs. Annexes I to V and Examples 1 to 4 illustrate the strategy used to select genus-specific, species-specific and universal PCR primers from *tuf* sequences or from the *recA* gene.

Oligonucleotide primers and probes design and synthesis

The DNA fragments sequenced by us or selected from databases (GenBank and EMBL) were used as sources of oligonucleotides for diagnostic purposes. For this strategy, an array of suitable oligonucleotide primers or probes derived from a variety of genomic DNA fragments (size of more than 100 bp) selected from databases were tested for their specificity and ubiquity in PCR and hybridization assays as described later. It is important to note that the database sequences were selected based on their potential for being species-specific, genus-specific or universal for the detection of bacteria or fungi according to available sequence information and extensive analysis and that, in general, several candidate database sequences had to be tested in order to obtain the desired specificity, ubiquity and sensitivity.

Oligonucleotide probes and amplification primers derived from species-specific fragments selected from database sequences were synthesized using an automated DNA synthesizer (Perkin-Elmer Corp., Applied Biosystems Division). Prior to synthesis, all oligonucleotides (probes for hybridization and primers for DNA amplification) were evaluated for their suitability for hybridization or DNA amplification by polymerase chain reaction (PCR) by computer analysis using standard programs (i.e. the Genetics Computer Group (GCG) programs and the primer analysis software Oligo™ 4.0). The potential suitability of the PCR primer pairs was also evaluated prior to the synthesis by verifying the absence of unwanted features such as long stretches of one nucleotide and a high proportion of G or C residues at the 3' end (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

The oligonucleotide primers or probes may be derived from either strand of the duplex DNA. The primers or probes may consist of the bases A, G, C, or T or analogs and they may be degenerated at one or more chosen nucleotide position(s). The primers or probes may be of any suitable length and may be selected anywhere within the DNA sequences from proprietary fragments or from selected database sequences which are suitable for (i) the universal detection of bacteria, (ii) the species-specific detection and identification of *Enterococcus faecium*, *Listeria monocytogenes*, *Neisseria meningitidis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae* and *Candida albicans* (iii) the genus-specific detection of *Streptococcus* species, *Enterococcus* species, *Staphylococcus* species and *Neisseria* species or (iv) the detection of the 26 above-mentioned clinically important antibiotic resistance genes.

5 Variants for a given target bacterial gene are naturally occurring and are attributable to sequence variation within that gene during evolution (Watson *et al.*, 1987, Molecular Biology of the Gene, 4th ed., The Benjamin/Cummings Publishing Company, Menlo Park, CA; Lewin, 1989, Genes IV, John Wiley & Sons, New York, NY). For example, different strains of the same bacterial species may have a single or more nucleotide variation(s) at the oligonucleotide hybridization site. The person skilled in the art is well aware of the existence of variant bacterial or fungal DNA sequences for a specific gene and that the frequency of sequence variations depends on the selective pressure during evolution on a given gene product. The detection of a variant sequence for a region between two PCR primers may be demonstrated by sequencing the amplification product. In order to show the presence of sequence variants at the primer hybridization site, one has to amplify a larger DNA target with PCR primers outside that hybridization site. Sequencing of this larger fragment will allow the detection of sequence variation at this site. A similar strategy may be applied to show variants at the hybridization site of a probe. Insofar as the divergence of the target sequences or a part thereof does not affect the specificity and ubiquity of the amplification primers or probes, variant bacterial DNA is under the scope of this invention. Variants of the selected primers or probes may also be used to amplify or hybridize to a variant DNA.

20 **Sequencing of *tuf* sequences from a variety of bacterial and fungal species**

The nucleotide sequence of a portion of *tuf* genes was determined for a variety of bacterial and fungal species. The amplification primers SEQ ID NOs: 107 and 108, which amplify a *tuf* gene portion of approximately 890 bp, were used for the sequencing of bacterial *tuf* sequences. The amplification primers SEQ ID NOs: 109 and 172, which amplify a *tuf* gene portion of approximately 830 bp, were used for the sequencing of fungal *tuf* sequences. Both primer pairs can amplify *tufA* and *tufB* genes. This is not surprising because these two genes are nearly identical. For example, the entire *tufA* and *tufB* genes from *E. coli* differ at only 13 nucleotide positions (Neidhardt *et al.*, 1996, *Escherichia coli* and *Salmonella*: Cellular and Molecular Biology, 2nd ed., American Society for Microbiology Press, Washington, D.C.). These amplification primers are degenerated at several nucleotide positions and contain inosines in order to allow the amplification of a wide range of *tuf* sequences. The strategy used to select these amplification primers is similar to that illustrated in Annex I for the selection of universal primers. The amplification primers SEQ ID NOs: 107 and 108 could be used to amplify the *tuf* genes from any bacterial species. The amplification primers SEQ ID NOs: 109 and 172 could be used to amplify the *tuf* genes from any fungal species.

The *tuf* genes were amplified directly from bacterial or yeast cultures using the following amplification protocol: One μ L of cell suspension was transferred directly to

19 μ L of a PCR reaction mixture containing 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM $MgCl_2$, 1 μ M of each of the 2 primers, 200 μ M of each of the four dNTPs, 0.5 unit of *Taq* DNA polymerase (Promega Corp., Madison, WI). PCR reactions were subjected to cycling using a MJ Research PTC-200 thermal cycler (MJ Research Inc., Watertown, Mass.) as follows: 3 min at 96°C followed by 30-35 cycles of 1 min at 95°C for the denaturation step, 1 min at 30-50°C for the annealing step and 1 min at 72°C for the extension step. Subsequently, twenty microliters of the PCR-amplified mixture were resolved by electrophoresis in a 1.5% agarose gel. The gel was then visualized by staining with methylene blue (Flores *et al.*, 1992, Biotechniques, 13:203-205). The size of the amplification products was estimated by comparison with a 100-bp molecular weight ladder. The band corresponding to the specific amplification product (i.e. approximately 890 or 830 bp for bacterial or fungal *tuf* sequences, respectively) was excised from the agarose gel and purified using the QIAquick™ gel extraction kit (QIAGEN Inc., Chatsworth, CA). The gel-purified DNA fragment was then used directly in the sequencing protocol. Both strands of the *tuf* genes amplification product were sequenced by the dideoxynucleotide chain termination sequencing method by using an Applied Biosystems automated DNA sequencer (model 373A) with their PRISM™ Sequenase® Terminator Double-stranded DNA Sequencing Kit (Perkin-Elmer Corp., Applied Biosystems Division, Foster City, CA). The sequencing reactions were all performed by using the amplification primers (SEQ ID NOs: 107 to 109 and 172) and 100 ng per reaction of the gel-purified amplicon. In order to ensure that the determined sequence did not contain errors attributable to the sequencing of PCR artefacts, we have sequenced two preparations of the gel-purified *tuf* amplification product originating from two independent PCR amplifications. For all target microbial species, the sequences determined for both amplicon preparations were identical. Furthermore, the sequences of both strands were 100% complementary thereby confirming the high accuracy of the determined sequence. The *tuf* sequences determined using the above strategy are all in the Sequence Listing (i.e. SEQ ID NOs:118 to 146). Table 13 gives the originating microbial species and the source for each *tuf* sequence in the Sequence Listing.

The alignment of the *tuf* sequences determined by us or selected from databases reveals clearly that the length of the sequenced portion of the *tuf* genes is variable. There may be insertions or deletions of several amino acids. This explains why the size of the sequenced *tuf* amplification product was variable for both bacterial and fungal species. Among the *tuf* sequences determined by our group, we found insertions and deletions adding up to 5 amino acids or 15 nucleotides. Consequently, the nucleotide positions indicated on top of each of Annexes I to V do not correspond for *tuf* sequences having insertions or deletions.

It should also be noted that the various *tuf* sequences determined by us

occasionally contain degenerescences. These degenerated nucleotides correspond to sequence variations between *tufA* and *tufB* genes because the amplification primers amplify both *tuf* genes. These nucleotide variations were not attributable to nucleotide misincorporations by the *taq* DNA polymerase because the sequence of both strands were identical and also because the sequences determined with both preparations of the gel-purified *tuf* amplicons were identical.

The selection of amplification primers from *tuf* sequences

The *tuf* sequences determined by us or selected from databases were used to select PCR primers for (i) the universal detection of bacteria, (ii) the genus-specific detection and identification of *Enterococcus* spp. and *Staphylococcus* spp. and (iii) the species-specific detection and identification of *Candida albicans*. The strategy used to select these PCR primers was based on the analysis of multiple sequence alignments of various *tuf* sequences. For more details about the selection of PCR primers from *tuf* sequences, please refer to Examples 1 to 3 and Annexes I to IV.

The selection of amplification primers from *recA*

The comparison of the nucleotide sequence for the *recA* gene from various bacterial species including 5 species of streptococci allowed the selection of *Streptococcus*-specific PCR primers. For more details about the selection of PCR primers from *recA*, please refer to Example 4 and Annex V.

DNA fragment isolation from *Staphylococcus saprophyticus* by arbitrarily primed PCR

DNA sequences of unknown coding potential for the species-specific detection and identification of *Staphylococcus saprophyticus* were obtained by the method of arbitrarily primed PCR (AP-PCR).

AP-PCR is a method which can be used to generate specific DNA probes for microorganisms (Fani *et al.*, 1993, Mol. Ecol. 2:243-250). A description of the AP-PCR protocol used to isolate a species-specific genomic DNA fragment from *Staphylococcus saprophyticus* follows. Twenty different oligonucleotide primers of 10 nucleotides in length (all included in the AP-PCR kit OPAD (Operon Technologies, Inc., Alameda, CA)) were tested systematically with DNAs from 3 bacterial strains of *Staphylococcus saprophyticus* (all obtained from the American Type Culture Collection (ATCC): numbers 15305, 35552 and 43867) as well as with DNA from four other staphylococcal species (*Staphylococcus aureus* ATCC 25923, *Staphylococcus epidermidis* ATCC 14990, *Staphylococcus haemolyticus* ATCC 29970 and *Staphylococcus hominis* ATCC 35982). For all bacterial species, amplification was performed from a bacterial suspension adjusted to a standard 0.5 McFarland which corresponds to approximately 1.5×10^8 bacteria/mL. One μL of the standardized bacterial suspension was transferred directly to 19 μL of a PCR reaction mixture containing 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl_2 ,

1.2 μ M of only one of the 20 different AP-PCR primers OPAD, 200 μ M of each of the four dNTPs and 0.5 unit of *Taq* DNA polymerase (Promega Corp., Madison, WI). PCR reactions were subjected to cycling using a MJ Research PTC-200 thermal cycler (MJ Research Inc.) as follows: 3 min at 96°C followed by 35 cycles of 1 min at 95°C for the denaturation step, 1 min at 32°C for the annealing step and 1 min at 72°C for the extension step. A final extension step of 7 min at 72°C was made after the 35 cycles to ensure complete extension of PCR products. Subsequently, twenty microliters of the PCR amplified mixture were resolved by electrophoresis in a 2% agarose gel containing 0.25 μ g/mL of ethidium bromide. The size of the amplification products was estimated by comparison with a 50-bp molecular weight ladder.

Amplification patterns specific for *Staphylococcus saprophyticus* were observed with the AP-PCR primer OPAD-9 (SEQ ID NO: 25). Amplification with this primer consistently showed a band corresponding to a DNA fragment of approximately 450 bp for all *Staphylococcus saprophyticus* strains tested but not for any of the four other staphylococcal species tested. This species-specific pattern was confirmed by testing 10 more clinical isolates of *S. saprophyticus* selected from the culture collection of the microbiology laboratory of the CHUL as well as strains selected from the gram-positive bacterial species listed in Table 5.

The band corresponding to the approximately 450 bp amplicon which was specific and ubiquitous for *S. saprophyticus* based on AP-PCR was excised from the agarose gel and purified using the QIAquick™ gel extraction kit (QIAGEN Inc.). The gel-purified DNA fragment was cloned into the T/A cloning site of the pCR 2.1™ plasmid vector (Invitrogen Inc.) using T4 DNA ligase (New England BioLabs). Recombinant plasmids were transformed into *E. coli* DH5 α competent cells using standard procedures. Plasmid DNA isolation was done by the method of Birnboim and Doly (Nucleic Acids Res. 7:1513-1523) for small-scale preparations. All plasmid DNA preparations were digested with the *Eco*RI restriction endonuclease to ensure the presence of the approximately 450 bp AP-PCR insert into the recombinant plasmids. Subsequently, a large-scale and highly purified plasmid DNA preparation was performed from two selected clones shown to carry the AP-PCR insert by using the QIAGEN plasmid purification kit. These plasmid preparations were used for automated DNA sequencing.

Both strands of the AP-PCR insert from the two selected clones were sequenced by the dideoxynucleotide chain termination sequencing method with SP6 and T7 sequencing primers, by using an Applied Biosystems automated DNA sequencer as described previously. The analysis of the obtained sequences revealed that the DNA sequences for both strands from each clone were 100% complementary. Furthermore, it showed that the entire sequence determined for each clone were both identical. These sequencing data confirm the 100% accuracy for the determined 438

bp sequence (SEQ ID NO: 29). Optimal amplification primers have been selected from the sequenced AP-PCR *Staphylococcus saprophyticus* DNA fragment with the help of the primer analysis software Oligo™ 4.0. The selected primer sequences have been tested in PCR assays to verify their specificity and ubiquity (Table 7). These PCR primers were specific since there was no amplification with DNA from bacterial species other than *S. saprophyticus* selected from Tables 4 and 5. Furthermore, this assay was ubiquitous since 245 of 260 strains of *S. saprophyticus* were efficiently amplified with this PCR assay. When used in combination with another *S. saprophyticus*-specific PCR assay, which is an object of our co-pending U.S. (N.S. 08/526,840) and PCT (PCT/CA/95/00528) patent applications, the ubiquity reaches 100% for these 260 strains.

DNA amplification

For DNA amplification by the widely used PCR (polymerase chain reaction) method, primer pairs were derived from proprietary DNA fragments or from database sequences. Prior to synthesis, the potential primer pairs were analyzed by using the Oligo™ 4.0 software to verify that they are good candidates for PCR amplification.

During DNA amplification by PCR, two oligonucleotide primers binding respectively to each strand of the heat-denatured target DNA from the bacterial genome are used to amplify exponentially *in vitro* the target DNA by successive thermal cycles allowing denaturation of the DNA, annealing of the primers and synthesis of new targets at each cycle (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

Briefly, the PCR protocols were as follow: Treated clinical specimens or standardized bacterial or fungal suspensions (see below) were amplified in a 20 μ L PCR reaction mixture containing 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 2.5 mM MgCl₂, 0.4 μ M of each primer, 200 μ M of each of the four dNTPs and 0.5 unit of *Taq* DNA polymerase (Promega) combined with the TaqStart™ antibody (Clontech Laboratories Inc., Palo Alto, CA). The TaqStart™ antibody, which is a neutralizing monoclonal antibody to *Taq* DNA polymerase, was added to all PCR reactions to enhance the specificity and the sensitivity of the amplifications (Kellogg *et al.*, 1994, Biotechniques 16:1134-1137). The treatment of the clinical specimens varies with the type of specimen tested, since the composition and the sensitivity level required are different for each specimen type. It consists in a rapid protocol to lyse the bacterial cells and eliminate the PCR inhibitory effects (see example 11 for urine specimen preparation). For amplification from bacterial or fungal cultures, the samples were added directly to the PCR amplification mixture without any pre-treatment step (see example 10). Primer sequences derived from highly conserved regions of the bacterial 16S ribosomal RNA gene were used to provide an internal control for all PCR reactions. Alternatively, the

internal control was derived from sequences not found in microorganisms or in the human genome. The internal control was integrated into all amplification reactions to verify the efficiency of the PCR assays and to ensure that significant PCR inhibition was absent. The internal control derived from rRNA was also useful to monitor the efficiency of bacterial lysis protocols.

PCR reactions were then subjected to thermal cycling (3 min at 95°C followed by 30 cycles of 1 second at 95°C for the denaturation step and 30 second at 55°C for the annealing-extension step) using a PTC-200 thermal cycler (MJ Research Inc.) and subsequently analyzed by standard ethidium bromide-stained agarose gel electrophoresis. The number of cycles performed for the PCR assays varies according to the sensitivity level required. For example, the sensitivity level required for microbial detection directly from clinical specimens is higher for blood specimens than for urine specimens because the concentration of microorganisms associated with a septicemia can be much lower than that associated with a urinary tract infection. Consequently, more sensitive PCR assays having more thermal cycles are required for direct detection from blood specimens. Similarly, PCR assays performed directly from bacterial or fungal cultures may be less sensitive than PCR assays performed directly from clinical specimens because the number of target organisms is normally much lower in clinical specimens than in microbial cultures.

It is clear that other methods for the detection of specific amplification products, which may be faster and more practical for routine diagnosis, may be used. Such methods may be based on the detection of fluorescence after amplification (e.g. TaqMan™ system from Perkin Elmer or Amplisensor™ from Biotronics). Methods based on the detection of fluorescence are particularly promising for utilization in routine diagnosis as they are very rapid, quantitative and can be automated (Example 14).

Microbial pathogens detection and identification may also be performed by solid support or liquid hybridization using species-specific internal DNA probes hybridizing to an amplification product. Such probes may be generated from any species-specific or genus-specific DNA amplification products which are objects of the present invention. Alternatively, the internal probes for species or genus detection and identification may be derived from the amplicons produced by the universal amplification assay. The oligonucleotide probes may be labeled with biotin or with digoxigenin or with any other reporter molecules.

To assure PCR efficiency, glycerol, dimethyl sulfoxide (DMSO) or other related solvents can be used to increase the sensitivity of the PCR and to overcome problems associated with the amplification of a target DNA having a high GC content or forming strong secondary structures (Dieffenbach and Dveksler, 1995, PCR Primer : A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, New York). The

concentration ranges for glycerol and DMSO are 5-15% (v/v) and 3-10% (v/v), respectively. For the PCR reaction mixture, the concentration ranges for the amplification primers and MgCl_2 are 0.1-1.5 μM and 1.5-3.5 mM, respectively. Modifications of the standard PCR protocol using external and nested primers (i.e. nested PCR) or using more than one primer pair (i.e. multiplex PCR) may also be used (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). For more details about the PCR protocols and amplicon detection methods, see Examples 9 to 14.

The person skilled in the art of DNA amplification knows the existence of other rapid amplification procedures such as ligase chain reaction (LCR), transcription-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA), branched DNA (bDNA) and cycling probe technology (CPT) (Lee *et al.*, 1997, Nucleic Acid Amplification Technologies: Application to Disease Diagnosis, Eaton Publishing, Boston, MA ; Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). The scope of this invention is not limited to the use of amplification by PCR, but rather includes the use of any rapid nucleic acid amplification method or any other procedure which may be used to increase rapidity and sensitivity of the tests. Any oligonucleotide suitable for the amplification of nucleic acids by approaches other than PCR and derived from the species-specific, genus-specific and universal DNA fragments as well as from selected antibiotic resistance gene sequences included in this document are also under the scope of this invention.

Hybridization assays with oligonucleotide probes

In hybridization experiments, single-stranded oligonucleotides (size less than 100 nucleotides) have some advantages over DNA fragment probes for the detection of bacteria, such as ease of synthesis in large quantities, consistency in results from batch to batch and chemical stability. Briefly, for the hybridizations, oligonucleotides were 5' end-labeled with the radionucleotide $\gamma\text{-}^{32}\text{P(dATP)}$ using T4 polynucleotide kinase (Pharmacia) (Sambrook *et al.*, 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). The unincorporated radionucleotide was removed by passing the labeled oligonucleotide through a Sephadex G-50TM column. Alternatively, oligonucleotides were labeled with biotin, either enzymatically at their 3' ends or incorporated directly during synthesis at their 5' ends, or with digoxigenin. It will be appreciated by the person skilled in the art that labeling means other than the three above labels may be used.

Each oligonucleotide probe was then tested for its specificity by hybridization to DNAs from a variety of bacterial and fungal species selected from Tables 4, 5 and 6. All of the bacterial or fungal species tested were likely to be pathogens associated

with common infections or potential contaminants which can be isolated from clinical specimens. Each target DNA was released from bacterial cells using standard chemical treatments to lyse the cells (Sambrook *et al.*, 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). Subsequently, the DNA was denatured by conventional methods and then irreversibly fixed onto a solid support (e.g. nylon or nitrocellulose membranes) or free in solution. The fixed single-stranded target DNAs were then hybridized with the oligonucleotide probe cells (Sambrook *et al.*, 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). Pre-hybridization conditions were in 1 M NaCl + 10% dextran sulfate + 1% SDS + 100 μ g/mL salmon sperm DNA at 65°C for 15 min. Hybridization was performed in fresh pre-hybridization solution containing the labeled probe at 65°C overnight. Post-hybridization washing conditions were as follows: twice in 3X SSC containing 1% SDS, twice in 2X SSC containing 1% SDS and twice in 1X SSC containing 1% SDS (all of these washes were at 65°C for 15 min), and a final wash in 0.1X SSC containing 1% SDS at 25°C for 15 min. Autoradiography of washed filters allowed the detection of selectively hybridized probes. Hybridization of the probe to a specific target DNA indicated a high degree of similarity between the nucleotide sequence of these two DNAs because of the high stringency of the washes.

An oligonucleotide probe was considered specific only when it hybridized solely to DNA from the species or genus from which it was isolated. Oligonucleotide probes found to be specific were subsequently tested for their ubiquity (i.e. ubiquitous probes recognized most or all isolates of the target species or genus) by hybridization to microbial DNAs from clinical isolates of the species or genus of interest including ATCC strains. The DNAs from strains of the target species or genus were denatured, fixed onto nylon membranes and hybridized as described above. Probes were considered ubiquitous when they hybridized specifically with the DNA from at least 80% of the isolates of the target species or genus.

Specificity and ubiquity tests for oligonucleotide primers and probes

The specificity of oligonucleotide primers and probes, derived either from the DNA fragments sequenced by us or selected from databases, was tested by amplification of DNA or by hybridization with bacterial or fungal species selected from those listed in Tables 4, 5 and 6, as described in the two previous sections. Oligonucleotides found to be specific were subsequently tested for their ubiquity by amplification (for primers) or by hybridization (for probes) with bacterial DNAs from isolates of the target species or genus. Results for specificity and ubiquity tests with the oligonucleotide primers are summarized in Table 7. The specificity and ubiquity of the PCR assays using the selected amplification primer pairs were tested directly from cultures (see Examples 9 and 10) of bacterial or fungal species.

The various species-specific and genus-specific PCR assays which are objects of the present invention are all specific. For the PCR assays specific to bacterial species or genus, this means that DNA isolated from a wide variety of bacterial species, other than that from the target species or genus and selected from Tables 4 and 5, could not be amplified. For the PCR assay specific to *Candida albicans*, it means there was no amplification with genomic DNA from the fungal species listed in Table 6 as well as with a variety of bacterial species selected from Tables 4 and 5.

The various species-specific and genus-specific PCR assays which are objects of the present invention are also all ubiquitous (Table 7). (i) The species-specific PCR assays for *E. faecium*, *L. monocytogenes*, *S. saprophyticus*, *S. agalactiae* and *C. albicans* amplified genomic DNA from all or most strains of the target species tested, which were obtained from various sources and which are representative of the diversity within each target species (Table 7). The species identification of all of these strains was based on classical biochemical methods which are routinely used in clinical microbiology laboratories. (ii) The genus-specific PCR assays specific for *Enterococcus* spp., *Staphylococcus* spp., *Streptococcus* spp. and *Neisseria* spp. amplified genomic DNA from all or most strains of the target genus tested, which represent all clinically important bacterial species for each target genus. These strains were obtained from various sources and are representative of the diversity within each target genus. Again, the species identification of all of these strains was based on classical biochemical methods which are routinely used in clinical microbiology laboratories. More specifically, the four genus-specific PCR assays amplified the following species: (1) The *Enterococcus*-specific assay amplified efficiently DNA from all of the 11 enterococcal species tested including *E. avium*, *E. casseliflavus*, *E. dispar*, *E. durans*, *E. faecalis*, *E. faecium*, *E. flavescens*, *E. gallinarum*, *E. hirae*, *E. mundtii* and *E. raffinosus*. (2) The *Neisseria*-specific assay amplified efficiently DNA from all of the 12 neisserial species tested including *N. canis*, *N. cinerea*, *N. elongata*, *N. flavescens*, *N. gonorrhoeae*, *N. lactamica*, *N. meningitidis*, *N. mucosa*, *N. polysaccharea*, *N. sicca*, *N. subflava* and *N. weaveri*. (3) The *Staphylococcus*-specific assay amplified efficiently DNA from 13 of the 14 staphylococcal species tested including *S. aureus*, *S. auricularis*, *S. capitis*, *S. cohnii*, *S. epidermidis*, *S. haemolyticus*, *S. hominis*, *S. lugdunensis*, *S. saprophyticus*, *S. schleiferi*, *S. simulans*, *S. warneri* and *S. xylosus*. The staphylococcal species which could not be amplified is *S. sciuri*. (4) Finally, the *Streptococcus*-specific assay amplified efficiently DNA from all of the 22 streptococcal species tested including *S. agalactiae*, *S. anginosus*, *S. bovis*, *S. constellatus*, *S. crista*, *S. dysgalactiae*, *S. equi*, *S. gordonii*, *S. intermedius*, *S. mitis*, *S. mutans*, *S. oralis*, *S. parasanguis*, *S. pneumoniae*, *S. pyogenes*, *S. salivarius*, *S. sanguis*, *S. sabrinus*, *S. suis*, *S. uberis*, *S. vestibularis* and *S. viridans*. On the other hand, the *Streptococcus*-specific assay did not amplify 3 out of 9 strains

of *S. mutans* and 1 out of 23 strains of *S. salivarius*, thereby showing a slight lack of ubiquity for these two streptococcal species.

All specific and ubiquitous amplification primers for each target microbial species or genus or antibiotic resistance gene investigated are listed in Annex VI.

5 Divergence in the sequenced DNA fragments can occur, insofar as the divergence of these sequences or a part thereof does not affect the specificity of the probes or amplification primers. Variant bacterial DNA is under the scope of this invention.

The PCR amplification primers listed in Annex VI were all tested for their specificity and ubiquity using reference strains as well as clinical isolates from various
10 geographical locations. The 351 reference strains used to test the amplification and hybridization assays (Tables 4, 5 and 6) were obtained from (i) the American Type Culture Collection (ATCC): 85%, (ii) the Laboratoire de santé publique du Québec (LSPQ): 10%, (iii) the Centers for Disease Control and Prevention (CDC): 3% , (iv) the National Culture Type Collection (NCTC): 1% and (v) several other reference
15 laboratories throughout the world: 1%. These reference strains are representative of (i) 90 gram-negative bacterial species (169 strains; Table 4), (ii) 97 gram-positive bacterial species (154 strains; Table 5) and (iii) 12 fungal species (28 strains; Table 6).

Antibiotic resistance genes

Antimicrobial resistance complicates treatment and often leads to therapeutic
20 failures. Furthermore, overuse of antibiotics inevitably leads to the emergence of bacterial resistance. Our goal is to provide clinicians, in approximately one hour, the needed information to prescribe optimal treatments. Besides the rapid identification of negative clinical specimens with DNA-based tests for universal bacterial detection and the identification of the presence of a specific pathogen in the positive specimens with
25 species- and/or genus-specific DNA-based tests, clinicians also need timely information about the ability of the bacterial pathogen to resist antibiotic treatments. We feel that the most efficient strategy to evaluate rapidly bacterial resistance to antimicrobials is to detect directly from the clinical specimens the most common and clinically important antibiotic resistance genes (i.e. DNA-based tests for the detection
30 of antibiotic resistance genes). Since the sequence from the most important and common bacterial antibiotic resistance genes are available from databases, our strategy was to use the sequence from a portion or from the entire resistance gene to design specific oligonucleotide primers or probes which will be used as a basis for the development of rapid DNA-based tests. The sequence from each of the bacterial
35 antibiotic resistance genes selected on the basis of their clinical relevance (i.e. high incidence and importance) is given in the Sequence Listing. Tables 9 and 10 summarize some characteristics of the selected antibiotic resistance genes. Our approach is unique because the antibiotic resistance genes detection and the bacterial detection and identification are performed simultaneously in multiplex assays under

uniform PCR amplification conditions (Example 13).

Annex VI provides a list of all amplification primers selected from 26 clinically important antibiotic resistance genes which were tested in PCR assays. The various PCR assays for antibiotic resistance genes detection and identification were validated by testing several resistant bacterial isolates known to carry the targeted gene and obtained from various countries. The testing of a large number of strains which do not carry the targeted resistance gene was also performed to ensure that all assays were specific. So far, all PCR assays for antibiotic resistance genes are highly specific and have detected all control resistant bacterial strains known to carry the targeted gene. The results of some clinical studies to validate the array of PCR assays for the detection and identification of antibiotic resistance genes and correlate these DNA-based assays with standard antimicrobials susceptibility testing methods are presented in Tables 11 and 12.

Universal bacterial detection

In the routine microbiology laboratory, a high percentage of clinical specimens sent for bacterial identification are negative by culture (Table 4). Testing clinical samples with universal amplification primers or universal probes to detect the presence of bacteria prior to specific identification and screen out the numerous negative specimens is thus useful as it saves costs and may rapidly orient the clinical management of the patients. Several amplification primers and probes were therefore synthesized from highly conserved portions of bacterial sequences from the *tuf* genes (Table 8). The universal primer selection was based on a multiple sequence alignment constructed with sequences determined by us or selected from available database sequences as described in Example 1 and Annex I.

For the identification of database sequences suitable for the universal detection of bacteria, we took advantage of the fact that the complete genome sequences for two distant microorganisms (i.e. *Mycoplasma genitalium* and *Haemophilus influenzae*) are available. A comparison of the amino acid sequence for all proteins encoded by the genome of these two distant microorganisms led to the identification of highly homologous proteins. An analysis of these homologous proteins allowed to select some promising candidates for the development of universal DNA-based assays for the detection of bacteria. Since the complete nucleotide sequence of several other microbial genomes are presently available in databases, a person skilled in the art could arrive to the same conclusions by comparing genomes sequences other than those of *Mycoplasma genitalium* and *Haemophilus influenzae*. The selected *tuf* gene encodes a protein (EF-Tu) involved in the translation process during protein synthesis. Subsequently, an extensive nucleotide sequence analysis was performed with the *tuf* gene sequences available in databases as well as with novel *tuf* sequences which we have determined as described previously. All computer analysis of amino acid and

nucleotide sequences were performed by using the GCG programs. Subsequently, optimal PCR primers for the universal amplification of bacteria were selected with the help of the Oligo™ program. The selected primers are degenerated at several nucleotide positions and contain several inosines in order to allow the amplification of all clinically relevant bacterial species (Annex I). Inosine is a nucleotide analog able to specifically bind to any of the four nucleotides A, C, G or T. Degenerated oligonucleotides consist of an oligonucleotide mix having two or more of the four nucleotides A, C, G or T at the site of mismatches. The inclusion of inosine and/or degenerescences in the amplification primers allow mismatch tolerance thereby permitting the amplification of a wider array of target nucleotide sequences (Dieffenbach and Dveksler, 1995 PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, NY).

The amplification conditions with the universal primers were identical to those used for the species- and genus-specific amplification assays except that the annealing temperature was 50°C instead of 55°C. This universal PCR assay was specific and nearly ubiquitous for the detection of bacteria. The specificity for bacteria was verified by amplifying genomic DNA isolated from the 12 fungal species listed in Table 6 as well as genomic DNA from *Leishmania donovani*, *Saccharomyces cerevisiae* and human lymphocytes. None of the above eukaryotic DNA preparations could be amplified by the universal assay, thereby suggesting that this test is specific for bacteria. The ubiquity of the universal assay was verified by amplifying genomic DNAs from 116 reference strains which represent 95 of the most clinically relevant bacterial species. These species have been selected from the bacterial species listed in Tables 4 and 5. We found that 104 of these 116 strains could be amplified. The bacterial species which could not be amplified belong to the following genera: *Corynebacterium* (11 species) and *Stenotrophomonas* (1 species). Sequencing of the *tuf* genes from these bacterial species has been recently performed. This sequencing data has been used to select new universal primers which may be more ubiquitous. These primers are in the process of being tested. We also observed that for several species the annealing temperature had to be reduced to 45°C in order to get an efficient amplification. These bacterial species include *Gemella morbilbrum*, *Listeria* spp. (3 species) and *Gardnerella vaginalis*. It is important to note that the 95 bacterial species selected from Tables 4 and 5 to test the ubiquity of the universal assay include all of the most clinically relevant bacterial species associated with a variety of human infections acquired in the community or in hospitals (nosocomial infections). The most clinically important bacterial and fungal pathogens are listed in Tables 1 and 2.

EXAMPLES AND ANNEXES

The following examples and annexes are intended to be illustrative of the various methods and compounds of the invention, rather than limiting the scope thereof.

5 The various annexes show the strategies used for the selection of amplification primers from *tuf* sequences or from the *recA* gene: (i) Annex I illustrates the strategy used for the selection of the universal amplification primers from *tuf* sequences. (ii) Annex II shows the strategy used for the selection of the amplification primers specific for the genus *Enterococcus* from *tuf* sequences. (iii) Annex III illustrates the strategy
10 used for the selection of the amplification primers specific for the genus *Staphylococcus* from *tuf* sequences. (iv) Annex IV shows the strategy used for the selection of the amplification primers specific for the species *Candida albicans* from *tuf* sequences. (v) Annex V illustrates the strategy used for the selection of the amplification primers specific for the genus *Streptococcus* from *recA* sequences. (vi)
15 Annex VI gives a list of all selected primer pairs. As shown in these annexes, the selected amplification primers may contain inosines and/or degenerescences. Inosine is a nucleotide analog able to specifically bind to any of the four nucleotides A, C, G or T. Alternatively, degenerated oligonucleotides which consist of an oligonucleotide mix having two or more of the four nucleotides A, C, G or T at the site of mismatches
20 were used. The inclusion of inosine and/or of degenerescences in the amplification primers allow mismatch tolerance thereby permitting the amplification of a wider array of target nucleotide sequences (Dieffenbach and Dveksler, 1995 PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, New York).

EXAMPLES

25 EXAMPLE 1 :

Selection of universal PCR primers from *tuf* sequences. As shown in Annex I, the comparison of *tuf* sequences from a variety of bacterial and eukaryotic species allowed the selection of PCR primers which are universal for the detection of bacteria. The strategy used to design the PCR primers was based on the analysis of a multiple
30 sequence alignment of various *tuf* sequences. This multiple sequence alignment includes *tuf* sequences from 38 bacterial species and 3 eukaryotic species either determined by us or selected from databases (Table 13). A careful analysis of this multiple sequence alignment allowed the selection of primer sequences which are conserved within eubacteria but which discriminate sequences from eukaryotes,
35 thereby permitting the universal detection of bacteria. As shown in Annex I, the selected primers contain several inosines and degenerescences. This was necessary because there is a relatively high polymorphism among bacterial *tuf* sequences despite the fact that this gene is highly conserved. In fact, among the *tuf* sequences that we determined, we found many nucleotide variations as well as some deletions and/or

insertions of amino acids. The selected universal primers were specific and ubiquitous for bacteria (Table 7). Of the 95 most clinically important bacterial species tested, 12 were not amplified. These species belong to the genera *Corynebacterium* (11 species) and *Stenotrophomonas* (1 species). The universal primers did not amplify DNA of non-bacterial origin, including human and other types of eukaryotic DNA.

EXAMPLE 2 :

Selection of genus-specific PCR primers from *tuf* sequences. As shown in Annexes 2 and 3, the comparison of *tuf* sequences from a variety of bacterial species allowed the selection of PCR primers specific for *Enterococcus* spp. or for *Staphylococcus* spp. The strategy used to design the PCR primers was based on the analysis of a multiple sequence alignment of various *tuf* sequences. These multiple sequence alignments include the *tuf* sequences of four representative bacterial species selected from each target genus as well as *tuf* sequences from species of other closely related bacterial genera. A careful analysis of those alignments allowed the selection of oligonucleotide sequences which are conserved within the target genus but which discriminate sequences from other closely related genera, thereby permitting the genus-specific and ubiquitous detection and identification of the target bacterial genus.

For the selection of primers specific for *Enterococcus* spp. (Annex II), we have sequenced a portion of approximately 890 bp of the *tuf* genes for *Enterococcus avium*, *E. faecalis*, *E. faecium* and *E. gallinarum*. All other *tuf* sequences used in the alignment were either sequenced by us or selected from databases. The analysis of this sequence alignment led to the selection of a primer pair specific and ubiquitous for *Enterococcus* spp. (Table 7). All of the 11 enterococcal species tested were efficiently amplified and there was no amplification with genomic DNA from bacterial species of other genera.

For the selection of primers specific for *Staphylococcus* spp. (Annex III), we have also sequenced a portion of approximately 890 bp of the *tuf* genes for *Staphylococcus aureus*, *S. epidermidis*, *S. saprophyticus* and *S. simulans*. All other *tuf* sequences used in the alignment were either sequenced by us or selected from databases. The analysis of this sequence alignment led to the selection of two primer pairs specific and ubiquitous for *Staphylococcus* spp. (Table 7). Annex III shows the strategy used to select one of these two PCR primer pairs. The same strategy was used to select the other primer pair. Of the 14 staphylococcal species tested, one (*S. sciuri*) could not be amplified by the *Staphylococcus*-specific PCR assays using either one of these two primer pairs. For PCR assays using either one of these two primer pairs, there was no amplification with DNA from species of other bacterial genera.

EXAMPLE 3 :

Selection from *tuf* sequences of PCR primers specific for *Candida albicans*. As shown in Annex IV, the comparison of *tuf* sequences from a variety of bacterial and eukaryotic species allowed the selection of PCR primers specific for *Candida albicans*.
5 The strategy used to design the PCR primers was based on the analysis of a multiple sequence alignment of various *tuf* sequences. This multiple sequence alignment includes *tuf* sequences of five representative fungal species selected from the genus *Candida* which were determined by our group (i.e. *C. albicans*, *C. glabrata*, *C. krusei*, *C. parapsilosis* and *C. tropicalis*) as well as *tuf* sequences from other closely related
10 fungal species. *tuf* sequences from various bacterial species were also included. A careful analysis of this sequence alignment allowed the selection of primers from the *C. albicans* *tuf* sequence; these primers discriminate sequences from other closely related *Candida* species and other fungal species, thereby permitting the species-specific and ubiquitous detection and identification of *C. albicans* (Table 7). All of 88
15 *Candida albicans* strains tested were efficiently amplified and there was no amplification with genomic DNA from other fungal or bacterial species.

EXAMPLE 4:

Selection of PCR primers specific for *Streptococcus* from *recA*. As shown in Annex V, the comparison of the various bacterial *recA* gene sequences available from
20 databases (GenBank and EMBL) was used as a basis for the selection of PCR primers which are specific and ubiquitous for the bacterial genus *Streptococcus*. Since sequences of the *recA* gene are available for many bacterial species including five species of streptococci, it was possible to choose sequences well conserved within the genus *Streptococcus* but distinct from the *recA* sequences for other bacterial genera.
25 When there were mismatches between the *recA* gene sequences from the five *Streptococcus* species, an inosine residue was incorporated into the primer (Annex V). The selected primers, each containing one inosine and no degenerescence, were specific and ubiquitous for *Streptococcus* species (Table 7). This PCR assay amplified all of the 22 streptococcal species tested. However, the *Streptococcus*-specific assay
30 did not amplify DNA from 3 out of 9 strains of *S. mutans* and 1 out of 3 strains of *S. salivarius*. There was no amplification with genomic DNA from other bacterial genera (Table 7).

EXAMPLE 5:

Nucleotide sequencing of DNA fragments. The nucleotide sequence of a portion
35 of the *tuf* genes from a variety of bacterial or fungal species was determined by using the dideoxynucleotide chain termination sequencing method (Sanger *et al.*, 1977, Proc. Natl. Acad. Sci. USA. 74:5463-5467). The sequencing was performed by using an Applied Biosystems automated DNA sequencer (model 373A) with their PRISM™ Sequenase® Terminator Double-stranded DNA Sequencing Kit (Perkin-Elmer Corp.,

Applied Biosystems Division, Foster City, CA). The sequencing strategy does not discriminate *tufA* and *tufB* genes because the sequencing primers hybridize efficiently to both bacterial *tuf* genes. These DNA sequences are shown in the sequence listing (SEQ ID Nos: 118 to 146). The presence of several degenerated nucleotides in the various *tuf* sequences determined by our group (Table 13) corresponds to sequence variations between *tufA* and *tufB*.

Oligonucleotide primers and probes selection. Oligonucleotide probes and amplification primers were selected from the given proprietary DNA fragments or database sequences using the Oligo™ program and were synthesized with an automated ABI DNA synthesizer (Model 391, Perkin-Elmer Corp., Applied Biosystems Division) using phosphoramidite chemistry.

EXAMPLE 6 :

Labeling of oligonucleotides for hybridization assays. Each oligonucleotide was 5' end-labeled with γ -³²P (dATP) by the T4 polynucleotide kinase (Pharmacia) as described earlier. The label could also be non-radioactive.

Specificity test for oligonucleotide probes. All labeled oligonucleotide probes were tested for their specificity by hybridization to DNAs from a variety of bacterial and fungal species selected from Tables 4, 5 and 6 as described earlier. Species-specific or genus-specific probes were those hybridizing only to DNA from the microbial species or genus from which it was isolated. Oligonucleotide probes found to be specific were submitted to ubiquity tests as follows.

Ubiquity test for oligonucleotide probes. Specific oligonucleotide probes were then used in ubiquity tests with strains of the target species or genus including reference strains and other strains obtained from various countries and which are representative of the diversity within each target species or genus. Chromosomal DNAs from the isolates were transferred onto nylon membranes and hybridized with labeled oligonucleotide probes as described for specificity tests. The batteries of isolates constructed for each target species or genus contain reference ATCC strains as well as a variety of clinical isolates obtained from various sources. Ubiquitous probes were those hybridizing to at least 80% of DNAs from the battery of clinical isolates of the target species or genus.

EXAMPLE 7:

Same as example 6 except that a pool of specific oligonucleotide probes is used for microbial identification (i) to increase sensitivity and assure 100% ubiquity or (ii) to identify simultaneously more than one microbial species and/or genus. Microbial identification could be performed from microbial cultures or directly from any clinical specimen.

EXAMPLE 8:

Same as example 6 except that bacteria or fungi were detected directly from clinical samples. Any biological sample was loaded directly onto a dot blot apparatus and cells were lysed *in situ* for bacterial or fungal detection and identification. Blood samples should be heparinized in order to avoid coagulation interfering with their convenient loading on a dot blot apparatus.

EXAMPLE 9:

PCR amplification. The technique of PCR was used to increase the sensitivity and the rapidity of the assays. The sets of primers were tested in PCR assays performed directly from bacterial colonies or from a standardized bacterial suspension (see Example 10) to determine their specificity and ubiquity (Table 7). Examples of specific and ubiquitous PCR primer pairs are listed in Annex VI.

Specificity and ubiquity tests for amplification primers. The specificity of all selected PCR primer pairs was tested against DNAs from a variety of bacterial and fungal species selected from Tables 4, 5 and 6 as described earlier. Primer pairs found specific for each species or genus were then tested for their ubiquity to ensure that each set of primers could amplify at least 90% of DNAs from a battery of isolates of the target species or genus. The batteries of isolates constructed for each species contain reference ATCC strains and various clinical isolates from around the world which are representative of the diversity within each species or genus.

Standard precautions to avoid false positive PCR results should be taken (Kwok and Higuchi, 1989, Nature, **239**:237-238). Methods to inactivate PCR amplification products such as the inactivation by uracil-N-glycosylase may be used to control PCR carryover.

EXAMPLE 10:

Amplification directly from bacterial or yeast cultures. PCR assays were performed either directly from a bacterial colony or from a bacterial suspension, the latter being adjusted to a standard McFarland 0.5 (corresponds to approximately 1.5×10^8 bacteria/mL). In the case of direct amplification from a colony, a portion of a colony was transferred using a plastic rod directly into a 20 μ L PCR reaction mixture containing 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM $MgCl_2$, 0.4 μ M of each primer, 200 μ M of each of the four dNTPs and 0.5 unit of Taq DNA polymerase (Promega) combined with the TaqStart™ antibody (Clontech Laboratories Inc.). For the bacterial suspension, 1 μ L of the cell suspension was added to 19 μ L of the same PCR reaction mixture. For the identification from yeast cultures, 1 μ L of a standard McFarland 1.0 (corresponds to approximately 3.0×10^8 bacteria/mL) concentrated 100 times by centrifugation was added directly to the PCR reaction. This concentration step for yeast cells was performed because a McFarland 0.5 for yeast cells has approximately 200 times fewer cells than a McFarland 0.5 for bacterial cells.

PCR reactions were then subjected to thermal cycling (3 min at 95°C followed by 30 cycles of 1 second at 95°C for the denaturation step and 30 seconds at 55°C for the annealing-extension step) using a PTC-200 thermal cycler. PCR amplification products were then analyzed by standard agarose gel (2%) electrophoresis.

5 Amplification products were visualized in agarose gels containing 0.25 µg/mL of ethidium bromide under UV at 254 nm. The entire PCR assay can be completed in approximately one hour.

Primer sequences derived from highly conserved regions of the bacterial 16S ribosomal RNA gene were used to provide an internal control for all PCR reactions.

10 Alternatively, the internal control was derived from sequences not found in microorganisms or in the human genome. The internal control was integrated into all amplification reactions to verify the efficiency of the PCR assays and to ensure that significant PCR inhibition was absent. The internal control derived from rRNA was also useful to monitor the efficiency of the bacterial lysis protocols. The internal control and

15 the species-specific or genus-specific amplifications were performed simultaneously in multiplex PCR assays.

EXAMPLE 11:

Amplification directly from urine specimens. For PCR amplification performed directly from urine specimens, 1 µL of urine was mixed with 4 µL of a lysis solution

20 containing 500 mM KCl, 100 mM tris-HCl (pH 9.0), 1% triton X-100. After incubation for at least 15 minutes at room temperature, 1 µL of the treated urine specimen was added directly to 19 µL of the PCR reaction mixture. The final concentration of the PCR reagents was 50 mM KCl, 10 mM Tris (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 0.4 µM of each primer, 200 µM of each of the four dNTPs. In addition, each

25 µL reaction contained 0.5 unit of *Taq* DNA polymerase (Promega) combined with the TaqStart™ antibody (Clontech Laboratories Inc.).

Strategies for the internal control, PCR amplification and agarose gel detection of the amplicons are as previously described in example 10.

EXAMPLE 12:

30 Detection of antibiotic resistance genes. The presence of specific antibiotic resistance genes which are frequently encountered and clinically relevant is identified using the PCR amplification or hybridization protocols described previously. Specific oligonucleotides used as a basis for the DNA-based tests are selected from the antibiotic resistance gene sequences. These tests, which allow the rapid evaluation of

35 bacterial resistance to antimicrobial agents, can be performed either directly from clinical specimens, from a standardized bacterial suspension or from a bacterial colony and should complement diagnostic tests for the universal detection of bacteria as well as for the species-specific and genus-specific microbial detection and identification.

EXAMPLE 13:

Same as examples 10 and 11 except that assays were performed by multiplex PCR (i.e. using several pairs of primers in a single PCR reaction) to reach an ubiquity of 100% for the specific targeted pathogen(s). For more heterogeneous microbial species or genus, a combination of PCR primer pairs may be required to detect and identify all representatives of the target species or genus.

Multiplex PCR assays could also be used to (i) detect simultaneously several microbial species and/or genera or, alternatively, (ii) to simultaneously detect and identify bacterial and/or fungal pathogens and detect specific antibiotic resistance genes either directly from a clinical specimen or from bacterial cultures.

For these applications, amplicon detection methods should be adapted to differentiate the various amplicons produced. Standard agarose gel electrophoresis could be used because it discriminates the amplicons based on their sizes. Another useful strategy for this purpose would be detection using a variety of fluorescent dyes emitting at different wavelengths. The fluorescent dyes can be each coupled with a specific oligonucleotide linked to a fluorescence quencher which is degraded during amplification to release the fluorescent dyes (e.g. TaqMan™, Perkin Elmer).

EXAMPLE 14:

Detection of amplification products. The person skilled in the art will appreciate that alternatives other than standard agarose gel electrophoresis (Example 10) may be used for the revelation of amplification products. Such methods may be based on fluorescence polarization or on the detection of fluorescence after amplification (e.g. Amplisensor™, Biotronics; TaqMan™, Perkin-Elmer Corp.) or other labels such as biotin (SHARP Signal™ system, Digene Diagnostics). These methods are quantitative and may be automated. One of the amplification primers or an internal oligonucleotide probe specific to the amplicon(s) derived from the species-specific, genus-specific or universal DNA fragments is coupled with the fluorescent dyes or with any other label. Methods based on the detection of fluorescence are particularly suitable for diagnostic tests since they are rapid and flexible as fluorescent dyes emitting at different wavelengths are available.

EXAMPLE 15:

Species-specific, genus-specific, universal and antibiotic resistance gene amplification primers can be used in other rapid amplification procedures such as the ligase chain reaction (LCR), transcription-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA), cycling probe technology (CPT) and branched DNA (bDNA) or any other methods to increase the sensitivity of the test. Amplifications can be performed from isolated bacterial cultures or directly from any clinical specimen. The scope of this invention is therefore not limited to the use of the

DNA sequences from the enclosed Sequence Listing for PCR only but rather includes the use of any procedures to specifically detect bacterial DNA and which may be used to increase rapidity and sensitivity of the tests.

EXAMPLE 16:

- 5 A test kit would contain sets of probes specific for each microbial species or genus as well as a set of universal probes. The kit is provided in the form of test components, consisting of the set of universal probes labeled with non-radioactive labels as well as labeled species- or genus-specific probes for the detection of each pathogen of interest in specific types of clinical samples. The kit will also include test reagents necessary to perform the pre-hybridization, hybridization, washing steps and hybrid detection. Finally, test components for the detection of known antibiotic resistance genes (or derivatives therefrom) will be included. Of course, the kit will include standard samples to be used as negative and positive controls for each hybridization test.
- 10
- 15 Components to be included in the kits will be adapted to each specimen type and to detect pathogens commonly encountered in that type of specimen. Reagents for the universal detection of bacteria will also be included. Based on the sites of infection, the following kits for the specific detection of pathogens may be developed:
- A kit for the universal detection of bacterial or fungal pathogens from all clinical specimens which contains sets of probes specific for highly conserved regions of the microbial genomes.
 - A kit for the detection of microbial pathogens retrieved from urine samples, which contains 5 specific test components (sets of probes for the detection of *Enterococcus faecium*, *Enterococcus* species, *Staphylococcus saprophyticus*, *Staphylococcus* species and *Candida albicans*).
 - A kit for the detection of respiratory pathogens which contains 3 specific test components (sets of probes for the detection of *Staphylococcus* species, *Enterococcus* species and *Candida albicans*).
 - A kit for the detection of pathogens retrieved from blood samples, which contains 10 specific test components (sets of probes for the detection of *Streptococcus* species, *Streptococcus agalactiae*, *Staphylococcus* species, *Staphylococcus saprophyticus*, *Enterococcus* species, *Enterococcus faecium*, *Neisseria* species, *Neisseria meningitidis*, *Listeria monocytogenes* and *Candida albicans*). This kit can also be applied for direct detection and identification from blood cultures.
 - A kit for the detection of pathogens causing meningitis, which contains 5 specific test components (sets of probes for the detection of *Streptococcus* species, *Listeria monocytogenes*, *Neisseria meningitidis*, *Neisseria* species and *Staphylococcus* species).
- 20
- 25
- 30
- 35

- A kit for the detection of clinically important antibiotic resistance genes which contains sets of probes for the specific detection of at least one of the 26 following genes associated with antibiotic resistance: *bla_{tem}*, *bla_{rob}*, *bla_{shv}*, *bla_{oxa}*, *bla_Z*, *aadB*, *aacC1*, *aacC2*, *aacC3*, *aacA4*, *aac6'-IIa*, *ermA*, *ermB*, *ermC*, *mecA*, *vanA*, *vanB*, *vanC*,
5 *satA*, *aac(6')-aph(2'')*, *aad(6')*, *vat*, *vga*, *msrA*, *sul* and *int*.

- Other kits adapted for the detection of pathogens from skin, abdominal wound or any other clinically relevant infections may also be developed.

EXAMPLE 17:

Same as example 16 except that the test kits contain all reagents and controls
10 to perform DNA amplification assays. Diagnostic kits will be adapted for amplification by PCR (or other amplification methods) performed directly either from clinical specimens or from microbial cultures. Components required for (i) universal bacterial detection, (ii) species-specific and genus-specific bacterial and/or fungal detection and identification and (iii) detection of antibiotic resistance genes will be included.

15 Amplification assays could be performed either in tubes or in microtitration plates having multiple wells. For assays in plates, the wells will contain the specific amplification primers and control DNAs and the detection of amplification products will be automated. Reagents and amplification primers for universal bacterial detection will be included in kits for tests performed directly from clinical specimens. Components
20 required for species-specific and genus-specific bacterial and/or fungal detection and identification as well as for the simultaneous antibiotic resistance genes detection will be included in kits for testing directly from bacterial or fungal cultures as well as in kits for testing directly from any type of clinical specimen.

The kits will be adapted for use with each type of specimen as described in
25 example 16 for hybridization-based diagnostic kits.

EXAMPLE 18:

It is understood that the use of the probes and amplification primers described in this invention for bacterial and/or fungal detection and identification is not limited to clinical microbiology applications. In fact, we feel that other sectors could also benefit
30 from these new technologies. For example, these tests could be used by industries for quality control of food, water, air, pharmaceutical products or other products requiring microbiological control. These tests could also be applied to detect and identify bacteria or fungi in biological samples from organisms other than humans (e.g. other primates, birds, plants, mammals, farm animals, livestock and others). These
35 diagnostic tools could also be very useful for research purposes including clinical trials and epidemiological studies.

This invention has been described herein above, and it is readily apparent that modifications can be made thereto without departing from the spirit of this invention. These modifications are under the scope of this invention, as defined in the appended claims.

Table 1. Distribution (%) of nosocomial pathogens for various human infections in USA (1990-1992)¹.

	Pathogen	UTI ²	SSI ³	BSI ⁴	Pneumonia	CSF ⁵
5	<i>Escherichia coli</i>	27	9	5	4	2
	<i>Staphylococcus aureus</i>	2	21	17	21	2
	<i>Staphylococcus epidermidis</i>	2	6	20	0	1
	<i>Enterococcus faecalis</i>	16	12	9	2	0
	<i>Enterococcus faecium</i>	1	1	0	0	0
10	<i>Pseudomonas aeruginosa</i>	12	9	3	18	0
	<i>Klebsiella pneumoniae</i>	7	3	4	9	0
	<i>Proteus mirabilis</i>	5	3	1	2	0
	<i>Streptococcus pneumoniae</i>	0	0	3	1	18
	Group B <i>Streptococci</i>	1	1	2	1	6
15	Other <i>Streptococci</i>	3	5	2	1	3
	<i>Haemophilus influenzae</i>	0	0	0	6	45
	<i>Neisseria meningitidis</i>	0	0	0	0	14
	<i>Listeria monocytogenes</i>	0	0	0	0	3
	Other <i>Enterococci</i>	1	1	0	0	0
20	Other <i>Staphylococci</i>	2		8	13	20
	<i>Candida albicans</i>	9	3	5	5	0
	Other <i>Candida</i>	2		1	3	10
	<i>Enterobacter</i> spp.	5	7	4	12	2
	<i>Acinetobacter</i> spp.	1	1	2	4	2
25	<i>Citrobacter</i> spp.	2	1	1	1	0
	<i>Serratia marcescens</i>	1	1	1	3	1
	Other <i>Klebsiella</i>	1	1	1	2	1
	Others	0	6	4	5	0

30 ¹ Data recorded by the National Nosocomial Infections Surveillance (NNIS) from 80 hospitals (Emori and Gaynes, 1993, Clin. Microbiol. Rev., 6:428-442).

² Urinary tract infection.

³ Surgical site infection.

⁴ Bloodstream infection.

35 ⁵ Cerebrospinal fluid.

Table 2. Distribution (%) of bloodstream infection pathogens in Quebec (1995), Canada (1992), UK (1969-1988) and USA (1990-1992).

5	Organism	Quebec ¹	Canada ²	UK ³		USA ⁴
				Community-acquired	Hospital-acquired	Hospital-acquired
	<i>E. coli</i>	15.6	53.8	24.8	20.3	5.0
	<i>S. epidermidis</i> and other CoNS ⁵	25.8	NI ⁶	0.5	7.2	31.0
10	<i>S. aureus</i>	9.6	NI	9.7	19.4	16.0
	<i>S. pneumoniae</i>	6.3	NI	22.5	2.2	NR ⁷
	<i>E. faecalis</i>	3.0	NI	1.0	4.2	NR
	<i>E. faecium</i>	2.6	NI	0.2	0.5	NR
	<i>Enterococcus</i> spp.	NR	NI	NR	NR	9.0
15	<i>H. influenzae</i>	1.5	NR	3.4	0.4	NR
	<i>P. aeruginosa</i>	1.5	8.2	1.0	8.2	3.0
	<i>K. pneumoniae</i>	3.0	11.2	3.0	9.2	4.0
	<i>P. mirabilis</i>	NR	3.9	2.8	5.3	1.0
20	<i>S. pyogenes</i>	NR	NI	1.9	0.9	NR
	<i>Enterobacter</i> spp.	4.1	5.5	0.5	2.3	4.0
	<i>Candida</i> spp.	8.5	NI	NR	1.0	8.0
	Others	18.5	17.4 ⁸	28.7	18.9	19.0

25 ¹ Data obtained for 270 isolates collected at the Centre Hospitalier de l'Université Laval (CHUL) during a 5 month period (May to October 1995).

² Data from 10 hospitals throughout Canada representing 941 gram-negative bacterial isolates. (Chamberland *et al.*, 1992, Clin. Infect. Dis., **15**:615-628).

30 ³ Data from a 20-year study (1969-1988) for nearly 4000 isolates (Eykyn *et al.*, 1990, J. Antimicrob. Chemother., Suppl. C, **25**:41-58).

⁴ Data recorded by the National Nosocomial Infections Surveillance (NNIS) from 80 hospitals (Emori and Gaynes, 1993, Clin. Microbiol. Rev., **6**:428-442).

⁵ Coagulase-negative staphylococci.

⁶ NI, not included. This survey included only gram-negative species.

35 ⁷ NR, incidence not reported for these species or genera.

⁸ In this case, 17.4 stands for other gram-negative bacterial species.

Table 3. Distribution of positive and negative clinical specimens tested at the microbiology laboratory of the CHUL (February 1994 – January 1995).

	Clinical specimens and/or sites	No. of samples tested (%)	% of positive specimens	% of negative specimens
5	Urine	17,981 (54.5)	19.4	80.6
	Blood culture/marrow	10,010 (30.4)	6.9	93.1
	Sputum	1,266 (3.8)	68.4	31.6
	Superficial pus	1,136 (3.5)	72.3	27.7
10	Cerebrospinal fluid	553 (1.7)	1.0	99.0
	Synovial fluid	523 (1.6)	2.7	97.3
	Respiratory tract	502 (1.5)	56.6	43.4
	Deep pus	473 (1.4)	56.8	43.2
	Ears	289 (0.9)	47.1	52.9
15	Pleural and pericardial fluid	132 (0.4)	1.0	99.0
	Peritoneal fluid	101(0.3)	28.6	71.4
	Total:	32,966 (100.0)	20.0	80.0

Table 4. Gram-negative bacterial species (90) used to test the specificity of PCR primers and DNA probes (continues on next page).

	Bacterial species	Number of reference strains tested ^a	Bacterial species	Number of reference strains tested ^a
5	<i>Acinetobacter baumannii</i>	1	<i>Moraxella phenylpyruvica</i>	1
	<i>Acinetobacter lwoffii</i>	3	<i>Morganella morganii</i>	1
	<i>Actinobacillus lignieresii</i>	1	<i>Neisseria animalis</i>	1
	<i>Alcaligenes faecalis</i>	1	<i>Neisseria canis</i>	1
	<i>Alcaligenes odorans</i>	1	<i>Neisseria caviae</i>	1
10	<i>Alcaligenes xylosoxydans</i>		<i>Neisseria cinerea</i>	1
	subsp. <i>denitrificans</i>	1	<i>Neisseria cuniculi</i>	1
	<i>Bacteroides distasonis</i>	1	<i>Neisseria elongata</i>	1
			subsp. <i>elongata</i>	
	<i>Bacteroides fragilis</i>	1	<i>Neisseria elongata</i>	1
15			subsp. <i>glycoytica</i>	
	<i>Bacteroides ovatus</i>	1	<i>Neisseria flavescens</i>	1
	<i>Bacteroides</i>	1	<i>Neisseria flavescens</i>	1
	<i>thetaiotaomicron</i>		<i>Branham</i>	
	<i>Bacteroides vulgatus</i>	1	<i>Neisseria gonorrhoeae</i>	18
20	<i>Bordetella bronchiseptica</i>	1	<i>Neisseria lactamica</i>	1
	<i>Bordetella parapertussis</i>	1	<i>Neisseria meningitidis</i>	4
	<i>Bordetella pertussis</i>	2	<i>Neisseria mucosa</i>	2
	<i>Burkholderia cepacia</i>	1	<i>Neisseria polysaccharea</i>	1
	<i>Citrobacter amalonaticus</i>	1	<i>Neisseria sicca</i>	3
25	<i>Citrobacter diversus</i>	2	<i>Neisseria subflava</i>	3
	subsp. <i>koseri</i>			
	<i>Citrobacter freundii</i>	1	<i>Neisseria weaveri</i>	1
	<i>Comamonas acidovorans</i>	1	<i>Ochrobactrum antropi</i>	1
	<i>Enterobacter aerogenes</i>	1	<i>Pasteurella aerogenes</i>	1
30	<i>Enterobacter</i>	1	<i>Pasteurella multocida</i>	1
	<i>agglomerans</i>			
	<i>Enterobacter cloacae</i>	1	<i>Prevotella melaninogenica</i>	1
	<i>Escherichia coli</i>	9	<i>Proteus mirabilis</i>	3
	<i>Escherichia fergusonii</i>	1	<i>Proteus vulgaris</i>	1

	Bacterial species	Number of reference strains tested ^a	Bacterial species	Number of reference strains tested ^a
	<i>Escherichia hermannii</i>	1	<i>Providencia alcalifaciens</i>	1
	<i>Escherichia vulneris</i>	1	<i>Providencia rettgeri</i>	1
	<i>Flavobacterium meningosepticum</i>	1	<i>Providencia rustigianii</i>	1
5	<i>Flavobacterium indologenes</i>	1	<i>Providencia stuartii</i>	1
	<i>Flavobacterium odoratum</i>	1	<i>Pseudomonas aeruginosa</i>	14
	<i>Fusobacterium necrophorum</i>	2	<i>Pseudomonas fluorescens</i>	2
10	<i>Gardnerella vaginalis</i>	1	<i>Pseudomonas stutzeri</i>	1
	<i>Haemophilus haemolyticus</i>	1	<i>Salmonella arizonae</i>	1
	<i>Haemophilus influenzae</i>	12	<i>Salmonella choleraesuis</i>	1
	<i>Haemophilus parahaemolyticus</i>	1	<i>Salmonella gallinarum</i>	1
15	<i>Haemophilus parainfluenzae</i>	2	<i>Salmonella typhimurium</i>	3
	<i>Hafnia alvei</i>	1	<i>Serratia liquefaciens</i>	1
	<i>Kingella indologenes</i>	1	<i>Serratia marcescens</i>	1
20	subsp. <i>suttonella</i>			
	<i>Kingella kingae</i>	1	<i>Shewanella putida</i>	1
	<i>Klebsiella ornithinolytica</i>	1	<i>Shigella boydii</i>	1
	<i>Klebsiella oxytoca</i>	1	<i>Shigella dysenteriae</i>	1
	<i>Klebsiella pneumoniae</i>	8	<i>Shigella flexneri</i>	1
25	<i>Moraxella atlantae</i>	1	<i>Shigella sonnei</i>	1
	<i>Moraxella catarrhalis</i>	5	<i>Stenotrophomonas maltophilia</i>	1
	<i>Moraxella lacunata</i>	1	<i>Yersinia enterocolitica</i>	1
	<i>Moraxella osloensis</i>	1		

- 30 ^a Most reference strains were obtained from the American Type Culture Collection (ATCC). The other reference strains were obtained from (i) the Laboratoire de Santé Publique du Québec (LSPQ), (ii) the Center for Disease Control and Prevention (CDC) and (iii) the National Culture Type Collection (NCTC).

Table 5. Gram-positive bacterial species (97) used to test the specificity of PCR primers and DNA probes (continues on next page).

	Bacterial species	Number of reference strains tested ^a	Bacterial species	Number of reference strains tested ^a
5	<i>Abiotrophia adiacens</i>	1	<i>Micrococcus kristinae</i>	1
	<i>Abiotrophia defectiva</i>	1	<i>Micrococcus luteus</i>	1
	<i>Actinomyces israelii</i>	1	<i>Micrococcus lylae</i>	1
	<i>Clostridium perfringens</i>	1	<i>Micrococcus roseus</i>	1
	<i>Corynebacterium accolens</i>	1	<i>Micrococcus varians</i>	1
10	<i>Corynebacterium aquaticum</i>	1	<i>Peptococcus niger</i>	1
	<i>Corynebacterium bovis</i>	1	<i>Peptostreptococcus anaerobius</i>	1
	<i>Corynebacterium cervicis</i>	1	<i>Peptostreptococcus asaccharolyticus</i>	1
	<i>Corynebacterium diptheriae</i>	6	<i>Staphylococcus aureus</i>	10
15	<i>Corynebacterium flavescens</i>	1	<i>Staphylococcus auricularis</i>	1
	<i>Corynebacterium genitalium</i>	6	<i>Staphylococcus capitis</i> subsp. <i>urealyticus</i>	1
	<i>Corynebacterium jeikeium</i>	1	<i>Staphylococcus cohnii</i>	1
20	<i>Corynebacterium kutcheri</i>	1	<i>Staphylococcus epidermidis</i>	2
	<i>Corynebacterium matruchotii</i>	1	<i>Staphylococcus haemolyticus</i>	2
	<i>Corynebacterium minutissimum</i>	1	<i>Staphylococcus hominis</i>	2
25	<i>Corynebacterium mycetoides</i>	1	<i>Staphylococcus lugdunensis</i>	1
	<i>Corynebacterium pseudodiphtheriticum</i>	1	<i>Staphylococcus saprophyticus</i>	3
	<i>Corynebacterium pseudogenitalium</i>	6	<i>Staphylococcus schleiferi</i>	1
30	<i>Corynebacterium renale</i>	1	<i>Staphylococcus sciuri</i>	1
	<i>Corynebacterium striatum</i>	1	<i>Staphylococcus simulans</i>	1
	<i>Corynebacterium ulcerans</i>	1	<i>Staphylococcus warneri</i>	1

	Bacterial species	Number of reference strains tested ^a	Bacterial species	Number of reference strains tested ^a
	<i>Corynebacterium urealyticum</i>	1	<i>Staphylococcus xylosus</i>	1
	<i>Corynebacterium xerosis</i>	1	<i>Streptococcus agalactiae</i>	6
	<i>Enterococcus avium</i>	1	<i>Streptococcus anginosus</i>	2
5	<i>Enterococcus casseliflavus</i>	1	<i>Streptococcus bovis</i>	2
	<i>Enterococcus cecorum</i>	1	<i>Streptococcus constellatus</i>	1
	<i>Enterococcus dispar</i>	1	<i>Streptococcus crista</i>	1
	<i>Enterococcus durans</i>	1	<i>Streptococcus dysgalactiae</i>	1
10	<i>Enterococcus faecalis</i>	6	<i>Streptococcus equi</i>	1
	<i>Enterococcus faecium</i>	3	<i>Streptococcus gordonii</i>	1
	<i>Enterococcus flavescens</i>	1	Group C <i>Streptococci</i>	1
	<i>Enterococcus gallinarum</i>	3	Group D <i>Streptococci</i>	1
	<i>Enterococcus hirae</i>	1	Group E <i>Streptococci</i>	1
15	<i>Enterococcus mundtii</i>	1	Group F <i>Streptococci</i>	1
	<i>Enterococcus pseudoavium</i>	1	Group G <i>Streptococci</i>	1
	<i>Enterococcus raffinosus</i>	1	<i>Streptococcus intermedius</i>	1
	<i>Enterococcus saccharolyticus</i>	1	<i>Streptococcus mitis</i>	2
20	<i>Enterococcus solitarius</i>	1	<i>Streptococcus mutans</i>	1
	<i>Eubacterium lentum</i>	1	<i>Streptococcus oralis</i>	1
	<i>Gemella haemolysans</i>	1	<i>Streptococcus parasanguis</i>	1
	<i>Gemella morbillorum</i>	1	<i>Streptococcus pneumoniae</i>	6
25	<i>Lactobacillus acidophilus</i>	1	<i>Streptococcus pyogenes</i>	3
	<i>Listeria innocua</i>	1	<i>Streptococcus salivarius</i>	2
	<i>Listeria ivanovii</i>	1	<i>Streptococcus sanguis</i>	2
	<i>Listeria grayi</i>	1	<i>Streptococcus sobrinus</i>	1
	<i>Listeria monocytogenes</i>	3	<i>Streptococcus suis</i>	1
30	<i>Listeria murrayi</i>	1	<i>Streptococcus uberis</i>	1
	<i>Listeria seeligeri</i>	1	<i>Streptococcus vestibularis</i>	1
	<i>Listeria welshimeri</i>	1		

^a Most reference strains were obtained from the American Type Culture Collection (ATCC). The other reference strains were obtained from (i) the Laboratoire de Santé Publique du Québec (LSPQ), (ii) the Center for Disease Control and Prevention (CDC) and (iii) the National Culture Type Collection (NCTC).

Table 6. Fungal species (12) used to test the specificity of PCR primers and DNA probes.

	Fungal species	Number of reference strains tested ^a
5	<i>Candida albicans</i>	12
	<i>Candida glabrata</i>	1
	<i>Candida guilliermondii</i>	1
	<i>Candida kefyr</i>	3
10	<i>Candida krusei</i>	2
	<i>Candida lusitanae</i>	1
	<i>Candida parapsilosis</i>	2
	<i>Candida tropicalis</i>	3
	<i>Rhodotorula glutinis</i>	1
15	<i>Rhodotorula minuta</i>	1
	<i>Rhodotorula rubra</i>	1
	<i>Saccharomyces cerevisiae</i>	1

^a Most reference strains were obtained from (i) the American Type Culture Collection (ATCC) and (ii) the Laboratoire de Santé Publique du Québec (LSPQ).

Table 7. PCR assays developed for several clinically important bacterial and fungal pathogens (continues on next page).

	Organism	Primer Pair ^a	Amplicon	Ubiquity ^b	DNA amplification from	
		SEQ ID NO	size (bp)		culture ^c	specimens ^d
	<i>Enterococcus faecium</i>	1-2	216	79/80	+	+
5	<i>Listeria monocytogenes</i>	3-4	130	164/168 ^e	+	+
	<i>Neisseria meningitidis</i>	5-6	177	258/258	+	+
	<i>Staphylococcus saprophyticus</i>	7-8	149	245/260	+	NT
10	<i>Streptococcus agalactiae</i>	9-10	154	29/29	+	+
	<i>Candida albicans</i>	11-12	149	88/88	+	NT
	<i>Enterococcus</i> spp. (11 species) ^f	13-14	112	87/87	+	NT
15	<i>Neisseria</i> spp. (12 species) ^f	15-16	103	321/321	+	+
	<i>Staphylococcus</i> spp. (14 species)	17-18	192	13/14	+	NT
		19-20	221	13/14	+	NT
20	<i>Streptococcus</i> spp. (22 species) ^f	21-22	153	210/214 ^g	+	+
	Universal detection ^h (95 species) ⁱ	23-24	309	104/ 116 ⁱ	+	+

25 ^a All primer pairs are specific in PCR assays since no amplification was observed with DNA from the bacterial and fungal species other than the species of interest listed in Tables 4, 5 and 6.

^b Ubiquity was tested by using reference strains as well as strains from throughout the world, which are representative of the diversity within each target species or genus.

30 ^c For all primer pairs, PCR amplifications performed directly from a standardized microbial suspension (MacFarland) or from a colony were all specific and ubiquitous.

^d PCR assays performed directly from blood cultures, urine specimens or

cerebrospinal fluid. NT, not tested.

- e The four *L. monocytogenes* strains undetected are not clinical isolates. These strains were isolated from food and are not associated with a human infection.
- f The bacterial species tested include all those clinically relevant for each genus (Tables 4 and 5). All of these species were efficiently amplified by their respective genus-specific PCR assay, except for the *Staphylococcus*-specific assay, which does not amplify *S. sciuri*.
- g The *Streptococcus*-specific PCR assay did not amplify 3 out of 9 strains of *S. mutans* and 1 out of 3 strains of *S. salivarius*.
- h The primers selected for universal bacterial detection do not amplify DNA of non-bacterial origin, including human and other types of eukaryotic genomic DNA.
- i For the universal amplification, the 95 bacterial species tested represent the most clinically important bacterial species listed in Tables 4 and 5. The 12 strains not amplified are representatives of genera *Corynebacterium* (11 species) and *Stenotrophomonas* (1 species).

Table 8. Target genes for the various genus-specific, species-specific and universal amplification assays.

	Microorganisms	Gene	Protein encoded
20	<i>Candida albicans</i>	<i>tuf</i>	translation elongation factor EF-Tu
	<i>Enterococcus faecium</i>	<i>ddl</i>	D-alanine:D-alanine ligase
	<i>Listeria monocytogenes</i>	<i>actA</i>	actin-assembly inducing protein
	<i>Neisseria meningitidis</i>	<i>omp</i>	outer membrane protein
25	<i>Streptococcus agalactiae</i>	<i>cAMP</i>	cAMP factor
	<i>Staphylococcus saprophyticus</i>	unknown	unknown
	<i>Enterococcus</i> spp.	<i>tuf</i>	translation elongation factor EF-Tu
	<i>Neisseria</i> spp.	<i>asd</i>	ASA-dehydrogenase
30	<i>Staphylococcus</i> spp.	<i>tuf</i>	translation elongation factor EF-Tu
	<i>Streptococcus</i> spp.	<i>recA</i>	RecA protein
	Universal detection	<i>tuf</i>	translation elongation factor EF-Tu

Table 9. Antibiotic resistance genes selected for diagnostic purposes.

	Genes	SEQ ID NOs		Antibiotics	Bacteria ^a
		selected primers	originating fragment		
5	<i>bla_{oxa}</i>	49-50	110	β-lactams	<i>Enterobacteriaceae</i> , <i>Pseudomonadaceae</i>
	<i>blaZ</i>	51-52	111	β-lactams	<i>Enterococcus</i> spp.
	<i>aac6'-IIa</i>	61-64	112	Aminoglycosides	<i>Pseudomonadaceae</i>
	<i>ermA</i>	91-92	113	Macrolides	<i>Staphylococcus</i> spp.
10	<i>ermB</i>	93-94	114	Macrolides	<i>Staphylococcus</i> spp.
	<i>ermC</i>	95-96	115	Macrolides	<i>Staphylococcus</i> spp.
	<i>vanB</i>	71-74	116	Vancomycin	<i>Enterococcus</i> spp.
	<i>vanC</i>	75-76	117	Vancomycin	<i>Enterococcus</i> spp.
15	<i>aad(6')</i>	173-174	-	Streptomycin	<i>Enterococcus</i> spp.

^a Bacteria having high incidence for the specified antibiotic resistance genes. The presence of these antibiotic resistance genes in other bacteria is not excluded.

Table 10. Antibiotic resistance genes from our co-pending US (N.S. 08/526840) and PCT (PCT/CA/95/00528) patent applications for which we have selected PCR primer pairs.

5	Genes	SEQ ID NOs	Antibiotics	Bacteria ^a
	of selected primers			
	<i>bla_{tem}</i>	37-40	β-lactams	<i>Enterobacteriaceae</i> , <i>Pseudomonadaceae</i> , <i>Haemophilus</i> spp., <i>Neisseria</i> spp.
	<i>bla_{rob}</i>	45-48	β-lactams	<i>Haemophilus</i> spp., <i>Pasteurella</i> spp.
10	<i>bla_{shv}</i>	41-44	β-lactams	<i>Klebsiella</i> spp. and other <i>Enterobacteriaceae</i>
	<i>aadB</i>	53-54	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonadaceae</i>
	<i>aacC1</i>	55-56		
	<i>aacC2</i>	57-58		
15	<i>aacC3</i>	59-60		
	<i>aacA4</i>	65-66		
	<i>mecA</i>	97-98	β-lactams	<i>Staphylococcus</i> spp.
	<i>vanA</i>	67-70	Vancomycin	<i>Enterococcus</i> spp.
	<i>satA</i>	81-82	Macrolides	<i>Enterococcus</i> spp.
20	<i>aac(6'')-aph(2'')</i>	83-86	Aminoglycosides	<i>Enterococcus</i> spp., <i>Staphylococcus</i> spp.
	<i>vat</i>	87-88	Macrolides	<i>Staphylococcus</i> spp.
	<i>vga</i>	89-90	Macrolides	<i>Staphylococcus</i> spp.
	<i>msrA</i>	77-80	Erythromycin	<i>Staphylococcus</i> spp.
25	<i>int</i>	99-102	β-lactams, trimethoprim,	<i>Enterobacteriaceae</i> ,
	<i>sul</i>	103-106	aminoglycosides, antiseptic, chloramphenicol	<i>Pseudomonadaceae</i>

^a Bacteria having high incidence for the specified antibiotic resistance genes. The presence of these antibiotic resistance genes in other bacteria is not excluded.

Table 11. Correlation between disk diffusion and PCR amplification of antibiotic resistance genes in *Staphylococcus* species^a.

				Disk diffusion (Kirby-Bauer) ^b		
	Antibiotic	Phenotype	PCR	Resistant	Intermediate	Sensitive
5	Penicillin	<i>blaZ</i>	+	165	0	0
			-	0	0	31
	Oxacillin	<i>mecA</i>	+	51	11	4
			-	2	0	128
10	Gentamycin	<i>aac(6')aph(2'')</i>	+	24	18	6
			-	0	0	148
	Erythromycin	<i>ermA</i>	+	15	0	0
		<i>ermB</i>	+	0	0	0
<i>ermC</i>		+	43	0	0	
15		<i>msrA</i>	+	4	0	0
			-	0	1	136

^a The *Staphylococcus* strains studied include *S. aureus* (82 strains), *S. epidermidis* (83 strains), *S. hominis* (2 strains), *S. capitis* (3 strains), *S. haemolyticus* (9 strains), *S. simulans* (12 strains) and *S. warneri* (5 strains), for a total of 196 strains.

^b Susceptibility testing was performed by the method of Kirby-Bauer according to the protocol recommended by the National Committee of Clinical Laboratory Standards (NCCLS).

Table 12. Correlation between disk diffusion profiles and PCR amplification of antibiotic resistance genes in *Enterococcus* species^a.

	Antibiotic	Phenotype	PCR	Disk diffusion (Kirby-Bauer) ^b	
				Resistant	Sensitive
5	Ampicillin	<i>blaZ</i>	+	0	2
			-	1	30
	Gentamycin	<i>aac(6')aph(2'')</i>	+	51	1
			-	3	38
10	Streptomycin	<i>aad(6')</i>	+	26	15
			-	6	27
	Vancomycin	<i>vanA</i>	+	36	0
		<i>vanB</i>	+	26	0
			-	0	40

15

^a The *Enterococcus* strains studied include *E. faecalis* (33 strains) and *E. faecium* (69 strains), for a total of 102 strains.

^b Susceptibility testing was performed by the method of Kirby-Bauer according to the protocol recommended by the National Committee of Clinical Laboratory Standards (NCCLS).

20

Table 13. Origin of *tuf* sequences in the Sequence Listing (continues on next page).

	SEQ ID NO	Bacterial or fungal species	Source
5	118	<i>Abiotrophia adiacens</i>	This patent
	119	<i>Abiotrophia defectiva</i>	This patent
	120	<i>Candida albicans</i>	This patent
	121	<i>Candida glabrata</i>	This patent
	122	<i>Candida krusei</i>	This patent
10	123	<i>Candida parapsilosis</i>	This patent
	124	<i>Candida tropicalis</i>	This patent
	125	<i>Corynebacterium accolens</i>	This patent
	126	<i>Corynebacterium diphtheriae</i>	This patent
	127	<i>Corynebacterium genitalium</i>	This patent
15	128	<i>Corynebacterium jeikeium</i>	This patent
	129	<i>Corynebacterium pseudotuberculosis</i>	This patent
	130	<i>Corynebacterium striatum</i>	This patent
	131	<i>Enterococcus avium</i>	This patent
	132	<i>Enterococcus faecalis</i>	This patent
20	133	<i>Enterococcus faecium</i>	This patent
	134	<i>Enterococcus gallinarum</i>	This patent
	135	<i>Gardnerella vaginalis</i>	This patent
	136	<i>Listeria innocua</i>	This patent
	137	<i>Listeria ivanovii</i>	This patent
25	138	<i>Listeria monocytogenes</i>	This patent
	139	<i>Listeria seeligeri</i>	This patent
	140	<i>Staphylococcus aureus</i>	This patent
	141	<i>Staphylococcus epidermidis</i>	This patent
	142	<i>Staphylococcus saprophyticus</i>	This patent
30	143	<i>Staphylococcus simulans</i>	This patent
	144	<i>Streptococcus agalactiae</i>	This patent
	145	<i>Streptococcus pneumoniae</i>	This patent

	SEQ ID NO	Bacterial or fungal species	Source
	146	<i>Streptococcus salivarius</i>	This patent
	147	<i>Agrobacterium tumefaciens</i>	Database
	148	<i>Bacillus subtilis</i>	Database
	149	<i>Bacteroides fragilis</i>	Database
5	150	<i>Borrelia burgdorferi</i>	Database
	151	<i>Brevibacterium linens</i>	Database
	152	<i>Burkholderia cepacia</i>	Database
	153	<i>Chlamydia trachomatis</i>	Database
	154	<i>Escherichia coli</i>	Database
10	155	<i>Fibrobacter succinogenes</i>	Database
	156	<i>Flavobacterium ferrugineum</i>	Database
	157	<i>Haemophilus influenzae</i>	Database
	158	<i>Helicobacter pylori</i>	Database
	159	<i>Micrococcus luteus</i>	Database
15	160	<i>Mycobacterium tuberculosis</i>	Database
	161	<i>Mycoplasma genitalium</i>	Database
	162	<i>Neisseria gonorrhoeae</i>	Database
	163	<i>Rickettsia prowazekii</i>	Database
	164	<i>Salmonella typhimurium</i>	Database
20	165	<i>Shewanella putida</i>	Database
	166	<i>Stigmatella aurantiaca</i>	Database
	167	<i>Streptococcus pyogenes</i>	Database
	168	<i>Thiobacillus cuprinus</i>	Database
	169	<i>Treponema pallidum</i>	Database
25	170	<i>Ureaplasma urealyticum</i>	Database
	171	<i>Wolinella succinogenes</i>	Database

Annex I: Strategy for the selection from *tuf* sequences of the universal amplification primers (continues on pages 49 to 51).

		SEQ ID
	491	NO
5	<i>Abiotrophia</i>	802
	<i>adiacens</i>	118
	<i>Abiotrophia</i>	119
	<i>defectiva</i>	147
	<i>Agrobacterium</i>	148
10	<i>tumefaciens</i>	149
	<i>Bacillus</i>	150
	<i>subtilis</i>	151
	<i>Bacteroides</i>	152
	<i>fragilis</i>	153
15	<i>Borrelia</i>	154
	<i>burgdorferi</i>	155
	<i>Brevibacterium</i>	156
	<i>linens</i>	157
20	<i>Burkholderia</i>	158
	<i>cepacia</i>	159
	<i>Chlamydia</i>	160
	<i>trachomatis</i>	161
	<i>Corynebacterium</i>	162
	<i>diphtheriae</i>	163

5	Corynebacterium genitalium	CCACCGTTAC CTCCATCGAG ATGTTCA...AGATGGT TATGCCGGGC GACAAGGTTG	127
	Corynebacterium jeikeium	CCACCGTTAC CTCCATCGAG ATGTTCA...AGATGGT TATGCCGGGC GACAAGGTTG	128
	Enterococcus faecalis	CAACYGTTAC AGGTGTTGAA ATGTTCC...AAATGGT AATGCCTGGT GATAACGTTG	132
	Enterococcus faecium	CAACAGTTAC TGGTGTGAA ATGTTCC...AAATGGT CATGCCCGGT GACAACGT..	133
	Escherichia coli	CTACCTGTAC TGGCGTTGAA ATGTTCC...AGATGGT AATGCCGGGC GACAACATCA	154
10	Fibrobacter succinogenes	ACGTATCAC CGGTGTTGAA ATGTTCC...AAATGGT TACTCCGGGT GACAAGGTTCA	155
	Flavobacterium ferrugineum	CTACCGTTAC AGGTGTTGAG ATGTTCC...AAATGGT TATGCCCTGGT GATAACACCA	156
	Gardnerella vaginalis	CCACCGTCAC CTCTATCGAG ACCTTCC...AAATGGT TCAGCCAGGC GATCAGCCAA	135
	Haemophilus influenzae	CTACTGTAAC GGGTGTGAA ATGTTCC...AAATGGT AATGCCAGGC GATAACATCA	157
	Helicobacter pylori	CGACTGTAAC CGGTGTAGAA ATGTTTA...AAATGGT TATGCCCTGGC GATAATGTGA	158
20	Listeria monocytogenes	TAGTAGTAAC TGGAGTAGAA ATGTTCC...AAATGGT AAYGCCTGGT GATAACATTG	138
	Micrococcus luteus	CCACTGTAC CGGCATCGAG ATGTTCC...AGATGGT CATGCCCGGC GACAACACCG	159
	Mycobacterium tuberculosis	CCACCGTCAC CGGTGTGAG ATGTTCC...AGATGGT GATGCCCGGT GACAACACCA	160

- 50 -

161	<u>CAGTTGTTAC</u> <u>TGGAATTGAA</u> <u>ATGTTCA...</u> <u>AAATGGT</u> <u>TCTACCTGGT</u> <u>GATAATGCTT</u>
162	<u>CCACCTGTAC</u> <u>CGGCGTTGAA</u> <u>ATGTTCC...</u> <u>AAATGGT</u> <u>AATGCCGGGT</u> <u>GAGAACGTAA</u>
163	<u>CCACTTGTAC</u> <u>AGGTGTAGAA</u> <u>ATGTTCA...</u> <u>AGATGGT</u> <u>TATGCCCTGGA</u> <u>GATAATGCTA</u>
164	<u>CTACCTGTAC</u> <u>TGGCGTTGAA</u> <u>ATGTTCC...</u> <u>AGATGGT</u> <u>AATGCCGGGC</u> <u>GACAAACATCA</u>
165	<u>CAACGTGTAC</u> <u>TGGTGTAGAA</u> <u>ATGTTCC...</u> <u>AGATGGT</u> <u>AATGCCAGGC</u> <u>GATAACATCA</u>
166	<u>CGGTCAATCAC</u> <u>GGGGTGGAG</u> <u>ATGTTCC...</u> <u>AGATGGT</u> <u>GATGCCGGGA</u> <u>GACAAACATCG</u>
140	<u>CAACTGTTAC</u> <u>AGGTGTGAA</u> <u>ATGTTCC...</u> <u>AAATGGT</u> <u>AATGCCCTGT</u> <u>GATAACGTTG</u>
141	<u>CAACTGTTAC</u> <u>TGGTGTAGAA</u> <u>ATGTTCC...</u> <u>AAATGGT</u> <u>TATGCCCTGGC</u> <u>GACAAACGTTG</u>
144	<u>CAGTTGTTAC</u> <u>TGGTGTGAA</u> <u>ATGTTCC...</u> <u>AAATGGT</u> <u>TATGCCCTGT</u> <u>GATAACGTTA</u>
145	<u>CAGTTGTTAC</u> <u>TGGTGTGAA</u> <u>ATGTTCC...</u> <u>AAATGGT</u> <u>AATGCCCTGT</u> <u>GATAACGTGA</u>
167	<u>CTGTTGTTAC</u> <u>TGGTGTGAA</u> <u>ATGTTCC...</u> <u>AAATGGT</u> <u>TATGCCCTGT</u> <u>GATAACGTGA</u>
168	<u>CCACCTGCAC</u> <u>CGGCGTTGAA</u> <u>ATGTTCA...</u> <u>AAATGGT</u> <u>CATGCCCGGC</u> <u>GATAATGTGA</u>
169	<u>CAGTGGTTAC</u> <u>TGGCAATGAG</u> <u>ATGTTTA...</u> <u>ACATGGT</u> <u>GAAGCCGGGG</u> <u>GATAACACCA</u>

- 51 -

Ureaplasma	CTGTGTGTTAC AGGAATGAA ATGTTTA...ATTGGT TATGCCAGGT GATGACGTTG	170
urealyticum		
Molinitella	CAACCGTAAC TGGCGTTGAG ATGTTCC...AGATGGT TATGCCTGGT GACAACGTTA	171
succinogenes		
5 Candida	GTGTACCAC TGAAGTCAAR TCCGTTG...AGRAATT GGAAGAAAT CCAAAATTCG	120
albicans		
Schizo-	GTGTCACTAC CGAAGTCAAG TCTGTTG...ACAAGAT TGAGGAGTCC CCTAAGTTTG	
saccharomyces pombe		
Human	TGACAGGCAT TGAGATGTTT CACAAGA...ACAAGAGCTTGCCATG CCGGGGAGG	
10 Selected ^a	ACIKKIAC IGGIGTIGAR ATGTT ATGGT IATGCCIGGI GAIAAYRT	
equences ^a		
Selected	SEQ ID NO:23	SEQ ID NO: 24 ^b
universal		
15 primer	ACIKKIAC IGGIGTIGAR ATGTT AYRTT ITCICCIGGC ATTACCAT	
sequences ^a :		

The sequence numbering refers to the *E. coli* tuf gene fragment. Underlined nucleotides are identical to the selected sequence or match that sequence.

20 ^a "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T. "K", "R" and "Y" designate nucleotide positions which are degenerated. "K" stands for T or G; "R" stands for A or G; "Y" stands for C or T.

^b This sequence is the reverse complement of the above tuf sequence.

Annex II: Strategy for the selection from *tuf* sequences of the amplification primers specific for the genus *Enterococcus* (continues on pages 53 and 54).

	314	348	401	435	SEQ ID NO
5 <i>Bacillus subtilis</i>	CGCGACACTG <u>AAAAACCAT</u>	CATGATGCCA GTTGA...CGCGG	ACAAGTTAAA	<u>GTCGCTGACG</u> <u>AAGTTGAAAT</u>	148
<i>Bacteroides fragilis</i>	CGCGATGTTG <u>ATAAACCTTT</u>	CTTGATGCCG GTAGA...ACTGG	TGTTATCCAT	<u>GTAGGTGATG</u> <u>AAATCGAAAT</u>	149
<i>Burkholderia cepacia</i>	CGTGCAGTTG <u>ACGCGCGGTT</u>	CCTGATGCCG GTGGA...CGCGG	CATCGTGAAG	<u>GTCGCGGAG</u> <u>AAATCGAAAT</u>	152
<i>Chlamydia trachomatis</i>	AGAGAAATTG <u>ACAAGCCTTT</u>	CTTAATGCCT ATTGA...CGTGG	AATTGTTAAA	<u>GTTTCCGATA</u> <u>AAGTTCAGTT</u>	153
<i>Corynebacterium diptheriae</i>	CGTGAGACCG <u>ACAAGCCATT</u>	CCTCATGCCT ATCGA...CGTGG	CTCCCTGAAG	<u>GTCAACGAGG</u> <u>ACGTCGAGAT</u>	126
15 <i>Enterococcus avium</i>	CGTGATACTG <u>ACAAACCAT</u>	CATGATGCCA GTCGA...CGTGG	ACAAGTTTCGC	<u>GTTGGTGACG</u> <u>AAGTTGAAAT</u>	131
<i>Enterococcus faecalis</i>	CGTGATACTG <u>ACAAACCAT</u>	CATGATGCCA GTCGA...CGTGG	TGAAGTTTCGC	<u>GTTGGTGACG</u> <u>AAGTTGAAAT</u>	132
<i>Enterococcus faecium</i>	CGTGACAACG <u>ACAAACCAT</u>	CATGATGCCA GTTGA...CGTGG	ACAAGTTTCGC	<u>GTTGGTGACG</u> <u>AAGTTGAAAT</u>	133
<i>Enterococcus gallinarum</i>	CGTGATACTG <u>ACAAACCAT</u>	CATGATGCCA GTCGA...CGTGG	ACAAGTTTCGC	<u>GTTGGTGATG</u> <u>AAGTAGAAT</u>	134
<i>Escherichia coli</i>	CGTGGGATTG <u>ACAAGCCGTT</u>	CCTGCTGCCG ATCGA...CGCGG	TATCATCAAA	<u>GTTGGTGAAG</u> <u>AAGTTGAAAT</u>	154

Gardnerella vaginalis	CACGATCTTG <u>ACAAGCCATT</u> CTTGATGCCA ATCGA...CGTGG TAAGCTCCCA ATCAACACACC CAGTTGAGAT	135
Haemophilus influenzae	CGTGCGATTG <u>ACCAACCGTT</u> CCTTCTTCCA ATCGA...CGAGG TATTATCCGT ACAGGTGATG AAGTAGAAAT	157
5 Helicobacter pylori	AGAGACACTG <u>AAAAAACTTT</u> CTTGATGCCG GTTGA...AGAGG CGTGGTGAAA GTAGGCGATG AAGTGGAAAT	158
Listeria monocytogenes	CGTGATACTG <u>ACAAACCATT</u> CATGATGCCA GTTGA...CGTGG ACAAGTTAAA GTTGTGACG AAGTAGAAGT	138
Micrococcus luteus	CGCGACAAGG <u>ACAAGCCGTT</u> CCTGATGCCG ATCGA...CGCGG CACCCTGAAG ATCAACTCCG AGTTCGAGAT	159
Mycobacterium tuberculosis	CGCGAGACCG <u>ACAAGCCGTT</u> CCTGATGCCG GTCGA...CGCGG CGTGATCAAC GTGACGAGG AAGTTGAGAT	160
Mycoplasma genitalium	CGTGAAGTAG <u>ATAAACCTTT</u> CTTATTAGCA ATTGA...AGAGG TGAAC TCAA GTAGTCAAG AAGTTGAAAT	161
15 Neisseria gonorrhoeae	CGTGCCGTGG <u>ACAAACCATT</u> CCTGCTGCCT ATCGA...CGAGG TATCATCCAC GTTGTGACG AGATTGAAAT	162
Salmonella typhimurium	CGTGCGATTG <u>ACAAGCCGTT</u> CCTGCTGCCG ATCGA...CGCGG TATCATCAAA GTGGCGAAG AAGTTGAAAT	164
Shewanella putida	CGTGACATCG <u>ATAAGCCGTT</u> CCTACTGCCA ATCGA...CGTGG TATTGTACGC GTAGGCGACG AAGTTGAAAT	165
20 Staphylococcus aureus	CGTGATTCTG <u>ACAAACCATT</u> CATGATGCCA GTTGA...CGTGG TCAAATCAAA GTTGTGAAG AAGTTGAAAT	140
Staphylococcus epidermidis	CGTGATTCTG <u>ACAAACCATT</u> CATGATGCCA GTTGA...CGTGG TCAAATCAAA GTWGTGAAG AAGTTGAAAT	141
25 Staphylococcus saprophyticus	CGTGATTCTG <u>ACAAACCATT</u> CATGATGCCA GTTGA...CGTGG TCAAATCAAA GTCGTGAAG AATCGARAT	142

Streptococcus CGTGATCTG ACAAACCTTT ACTTCTTCCA GTTGA...CGTGG TACTGTTTCGT GTCACGACG AAGTTGAAAT 144
agalactiae

Streptococcus CGTGACACTG ACAAACCAT GCTTCTTCCA GTCGA...CGTGG TATCGTTAAA GTCACGACG AAATCGAAAT 145
pneumoniae

5 Streptococcus CGCGACACTG ACAAACCAT GCTTCTTCCA GTCGA...CGTGG TACTGTTTCGT GTCACGACG AAATCGAAAT 167
pyogenes

Ureaplasma CGTAGTACTG ACAAACCAT CTTATTAGCA ATTGA...CGTGG TGTATTAAAA GTTAATGATG AGTTGAAAT 170
urealyticum

Selected TACTG ACAAACCAT CATGATG GTTCGC GTTGGTGACG AAGTT

10 sequences

Selected SEQ ID NO: 13 SEQ ID NO: 14^a

genus-specific

primer TACTG ACAAACCAT CATGATG AACTTC GTCACCAACG CGAAC

15 sequences:

The sequence numbering refers to the *E. faecalis* tuf gene fragment. Underlined nucleotides are identical to the selected sequence or match that sequence.

20 ^a This sequence is the reverse complement of the above tuf sequence.

NOTE: The above primers also amplify tuf sequences from Abiotrophia species; this genus has recently been related to the Enterococcus genus by 16S rRNA analysis.

Annex III: Strategy for the selection from *tuf* sequences of the amplification primers specific for the genus *Staphylococcus* (continues on pages 56 and 57).

	385	420.....579	611 SEQ ID
5 <i>Bacillus subtilis</i>	<u>TGGCCGTGTA</u>	<u>GAACGCGGAC</u> <u>AAGTTAAAGT</u> CGG.....TTG <u>CTAAACCAGG</u> <u>TACAATCACT</u> <u>CCACACAGCA</u>	148
<i>Bacteroides fragilis</i>	<u>AGGTCGTATC</u>	<u>GAAACTGGTG</u> <u>TTATCCATGT</u> AGG.....TTT <u>GTAACCCGGG</u> <u>TCAGATTAAA</u> <u>CCTCACTCTA</u>	149
<i>Burkholderia cepacia</i>	<u>GGGTCGTGTC</u>	<u>GAGCGCGGCA</u> <u>TCGTGAAGGT</u> CGG.....TGG <u>CGAAGCCGGG</u> <u>TTCCGATCAG</u> <u>CCGCACACGC</u>	152
10 <i>Chlamydia trachomatis</i>	<u>TGGACGTATT</u>	<u>GAGCGTGGAA</u> <u>TTGTTAAAGT</u> TTC.....TTT <u>GCTTGCAGAA</u> <u>CAGTGTAAA</u> <u>CCTCATACAC</u>	153
<i>Corynebacterium diptheriae</i>	<u>CGGCCGTGTT</u>	<u>GAGCGTGGCT</u> <u>CCCTGAAGGT</u> CAA.....TTG <u>TTAAGCCAGG</u> <u>CGCTTACACC</u> <u>GCTCACACCG</u>	126
15 <i>Enterococcus faecalis</i>	<u>AGGACGTGTT</u>	<u>GAACGTGGTG</u> <u>AAGTTCGCGT</u> TGG.....TAG <u>CTAAAGCAGC</u> <u>TACAATCACT</u> <u>CCACACACAA</u>	132
<i>Enterococcus faecium</i>	<u>AGGTCGTGTT</u>	<u>GAACGTGGAC</u> <u>AAGTTCGCGT</u> TGG.....TAG <u>CTAAACCAGG</u> <u>TACAATCACA</u> <u>CCTCQTACAA</u>	133
<i>Escherichia coli</i>	<u>CGGTCGTGTA</u>	<u>GAACGCGGTA</u> <u>TCATCAAAGT</u> TGG.....TGG <u>CTAAGCCGGG</u> <u>CACCATCAAG</u> <u>CCGCACACCA</u>	154
20 <i>Gardnerella vaginalis</i>	<u>CGGTCGTGTT</u>	<u>GAGCGTGGTA</u> <u>AGCTCCCAAT</u> CAA.....TGG <u>CTGCTCCAGG</u> <u>TTCTGTGACT</u> <u>CCACACACCA</u>	135

- 55 -

Haemophilus	AGGTCGTGTA	<u>GAACGAGGTA</u>	TTATCCGTAC	AGG.....TAG	CGAAACCCAGG	<u>TTCAATCACA</u>	<u>CCACACACTG</u>	157
influenzae								
Helicobacter	AGGTAGGATT	<u>GAAAGAGCG</u>	TGGTGAAGT	AGG.....TAT	GCAACCCAGG	<u>TTCTATCACT</u>	<u>CCGCACAAGA</u>	158
pylori								
5 Listeria	TGGACGTGTT	<u>GAACGTGGAC</u>	AAGTTAAAGT	TGG.....TAG	CTAAACCCAGG	<u>TTCGATTACT</u>	<u>CCACACACTA</u>	138
monocytogenes								
Micrococcus	CGGTCGCGCC	<u>GAGCGGCGCA</u>	CCCTGAAGAT	CAA.....TGG	TGGAGCCGGG	<u>CTCCATCACC</u>	<u>CCGCACACCA</u>	159
luteus								
Mycobacterium	CGGACGTGTG	<u>GAGCGGCGG</u>	TGATCAACGT	GAA.....TCA	CCAAGCCCGG	<u>CACCACCACG</u>	<u>CCGCACACCG</u>	160
10 tuberculosis								
Mycoplasma	AGGAAGAGTT	<u>GAAAGAGGTG</u>	AACTCAAAGT	AGG.....TAG	CAAAACCCAGG	<u>CTCTATTAAA</u>	<u>CCGCACAAGA</u>	161
genitalium								
Neisseria	CGGCCGTGTA	<u>GAGCGAGGTA</u>	TCATCCACGT	TGG.....TGG	CCAAACCCGGG	<u>TACTATCACT</u>	<u>CCTCACACCA</u>	162
gonorrhoeae								
15 Salmonella	CGGTCGTGTA	<u>GAGCGCGGTA</u>	TCATCAAAGT	GGG.....TGG	CTAAGCCGGG	<u>CACCATCAAG</u>	<u>CCGCACACCA</u>	164
typhimurium								
Shewanella	AGGTCGTGTT	<u>GAGCGTGGTA</u>	TTGTACGCGT	AGG.....TAG	CGAAGCCAGG	<u>TTCAATCAAC</u>	<u>CCACACACTA</u>	165
putida								
Staphylococcus	AGGCCGTGTT	<u>GAACGTGGTC</u>	AAATCAAAGT	TGG.....TAG	CTGCTCCTGG	<u>TTCAATTACA</u>	<u>CCACATACTG</u>	140
20 aureus								
Staphylococcus	AGGCCGTGTT	<u>GAACGTGGTC</u>	AAATCAAAGT	WGG.....TAG	CTGCTCCTGG	<u>TTCTATTACA</u>	<u>CCACACACAA</u>	141
epidermidis								
Staphylococcus	AGGCCGTGTT	<u>GAACGTGGTC</u>	AAATCAAAGT	CGG.....TAG	CTGCTCCTGG	<u>TACTATCACA</u>	<u>CCACATACAA</u>	142
saprophyticus								
25 Staphylococcus	AGGCCGTGTT	<u>GAACGTGGTC</u>	AAATCAAAGT	CGG.....TAG	CAGCTCCTGG	<u>CTCTATTACT</u>	<u>CCACACACAA</u>	143
simulans								

- 57 -

Streptococcus AGGACGTATC GACCGTGGTA CTGTTCGTGT CAA.....TTG CTAAACCAGG TTCAATCAAC CCACACACTA 144
 agalactiae

Streptococcus AGGACGTATC GACCGTGGTA TCGTTAAAGT CAA.....TCG CTAAACCAGG TTCAATCAAC CCACACACTA 145
 pneumoniae

5 Ureaplasma TGGACGTGTT GAACGTGGTG TATTAAAAAGT TAA.....TTG TAAACCAGG ATCAATTAAA CCTCACCGTA 170
 urealyticum

Selected CCGTGTT GAACGTGGTC AAATCAA GCTCCTGG YMCWATYACA CCACAYA

sequences^a

SEQ ID NO: 18^b

SEQ ID NO: 17

10 Selected

genus-specific

primer

sequences^a:

TRTGTGGT GTRATWGR CAGGAGC

CCGTGTT GAACGTGGTC AAATCAA

15 The sequence numbering refers to the *S.aureus* *tuf* gene fragment. Underlined nucleotides are identical to the selected sequence or match that sequence.

^a "R", "W" and "Y" designate nucleotide positions which are degenerated. "R" stands for A or G; "W", for A or T; "Y", for C or T.

20 ^b This sequence is the reverse complement of the above *tuf* sequence.

Annex IV: Strategy for the selection from tuf sequences of the amplification primers specific for the species *Candida albicans* (continues on pages 59 and 60).

58	90	181	213 SEQ ID NO
<i>Candida albicans</i>	CGTCAAGAAG GTTGGTTACA ACCCAAAGAC TGT...CAA ATCCGGTAAA GTTACTGGTA AGACCTTGTT	120	
<i>Candida glabrata</i>	CATCAAGAAG GTTCGGTTACA ACCCAAAGAC TGT...CAA GGCTGGTGTC GTCAAGGGTA AGAYCTTGTT	121	
<i>Candida krusei</i>	CATCAAGAAG GTTGGTTACA ACCCAAAGAC TGT...CAA GGCAAGGTGTT GTTAAGGGTA AGACCTTAAT	122	
<i>Candida parapsilosis</i>	CGTCAAGAAG GTTGGTTACA ACCCTAAAGC TGT...TAA AGCTGGTAAG GTTACCGGTA AGACCTTGTT	123	
<i>Candida tropicalis</i>	CGTCAAGAAG GTTGGTTACA ACCCTAAGGC TGT...CAA GGCTGGTAAG GTTACCGGTA AGACTTTTGTT	124	
<i>Schizosaccharomyces pombe</i>	CATCAAGAAG GTTCGGTTTCA ACCCCAAGAC CGT...CAA GGCTGGTGTC GTCAAGGGTA AGACTCTTTT	153	
Human	GGAGATCCGG GAGCTGCTCA CCGAGTTTGG CTA...GTT AGGCTGTAG TCTGTGCAGA AGCTACTGGA	126	
<i>Chlamydia trachomatis</i>	GGAGCTGCGC GAGCTGCTCA GCAAGTACGG CTT...CAA ATG..... TATTCTGG AGCTGATGAA	132	
<i>Corynebacterium diptheriae</i>	GGAGATCCRT GAGCTGCTCG CTGAGCAGGA TTA...GAA GTGGACCCAG TCCATCATCG ACCTCATGCA	154	
<i>Enterococcus faecalis</i>	GGAAGTTCGT GACTTATTAT CAGAAATACGA TTT..... TGAAGAA AAAATCTTAG AATTAATGGC		
<i>Escherichia coli</i>	GGAAGTTCGT GAACCTCTGT CTCAGTACGA CTT..... GGAAGCG AAAATCCTGG AACTGGCTGG		

Flavobacterium ferrugineum	CGAGGTTCCG <u>G</u> AAGAACTGA <u>C</u> TAAAGCGG TTT..... ..GGGTTAAA <u>G</u> AAATGAAA <u>A</u> CTGATGGA	156
Gardnerella vaginalis	AGAGGTCCTG <u>G</u> ACTCCTCG <u>A</u> AGAAAACGG CTT...CAA <u>G</u> TGGGTAGAG <u>A</u> CCGTCAAGG <u>A</u> ACTCATGAA	135
5 Haemophilus influenzae	GGAGTTTCGT <u>G</u> AACCTCTAT <u>C</u> TCAATATGA CTT..... ..GGGAAGAA <u>A</u> AAATCCTTG <u>A</u> GTAGCAAA	157
Listeria monocytogenes	GGAAATTTCGT <u>G</u> ATCTATTAA <u>C</u> TGAATATGA ATT..... ..GGGAAGCT <u>A</u> AAATGACG <u>A</u> GTAAATGGA	138
Micrococcus luteus	GGAGTCCGT <u>G</u> AGTTGCTG <u>C</u> TGCCAGGA ATT...CAA <u>G</u> TGGTCGAG <u>T</u> CTGTCAAC <u>A</u> GTGATGGA	159
Neisseria gonorrhoeae	GGAAATCCGC <u>G</u> ACTGCTGT <u>C</u> CAGCTACGA CTT..... ..ACGAAGAA <u>A</u> AAATCTTCG <u>A</u> ACTGGCTAC	162
Salmonella typhimurium	GGAGTTCGT <u>G</u> AACCTGCTGT <u>C</u> TCACTACGA CTT..... ..GGGAAGCG <u>A</u> AAATCATCG <u>A</u> ACTGGCTGG	164
15 Staphylococcus aureus	GGAGTTCGT <u>G</u> ACTTATTAA <u>G</u> CGAATATGA CTT..... ..CGAAGAA <u>A</u> AAATCTTAG <u>A</u> ATTAATGGA	140
Streptococcus pneumoniae	GGAAATCCGT <u>G</u> ACTATTGT <u>C</u> AGAATACGA CTT..... ..CGAAGAC <u>A</u> TCTTATGG <u>A</u> ATTGATGAA	145
Treponema pallidum	AGAGGTTCGT <u>G</u> ATCGCTTG <u>C</u> TGGATATGG GTT...GGA <u>G</u> GATGAGCT <u>T</u> GTATTGAGG <u>A</u> ACTGCTTGC	169

- 60 -

Selected sequences	<u>CAAGAAG GTTGGTTACA ACCCAAGA</u>	<u>ATCCGGTAAA GTTACTGGTA AGACCT</u>
Selected	SEQ ID NO: 11	SEQ ID NO: 12 ^a
5 species-specific primer	CAAGAAG GTTGGTTACA ACCCAAGA	AGGTCCTTACC AGTAACTTTAC CGGAT
sequences:		

10 The sequence numbering refers to the *Candida albicans* tuf gene fragment. Underlined nucleotides are identical to the selected sequence or match that sequence.

^a This sequence is the reverse-complement of the above tuf sequence.

Annex V: Strategy for the selection from the *recA* gene of the amplification primers specific for the genus *Streptococcus* (continues on pages 62 and 63).

	415	449...540	574 SEQ ID NO
5 <i>Bordetella</i>	CTCGAGATCA	CCGACGGCTT	GGTGGCTCG GGCTC...GGCCC GCCTGATGAG CCAGGCGCTG CGCAAGCTGA
<i>pertussis</i>			
<i>Burkholderia</i>	CTCGAAATCA	CCGATGGCTT	GGTGGCTCG GGCTC...GGCCC GCCTGATGTC GCAGGCGCTG CGCAAGCTGA
<i>cepacia</i>			
<i>Campylobacter</i>	TTAGAAATTG	TAGAAACTAT	AGCAAGAAGT GGCGC...AGCAA GACTTATGTC TCAAGCTCTA AGAAACTTAA
10 <i>jejuni</i>			
<i>Chlamydia</i>	TTGAGTATTG	CAGAGCTCTT	AGCGCGTTCT GGAGC...AGCTC GCATGATGTC GCAGGCTCTA CGCAAATTAA
<i>trachomatis</i>			
<i>Clostridium</i>	TTAGAAATTA	CAGAAAGCTT	AGTTAGATCA GGAGC...AGCTA GATTAATGTC ACAAGCCTTA AGAAAGTTAA
<i>perfringens</i>			
15 <i>Corynebacterium</i>	CTGGAGATTG	CAGATATGCT	TGTTGGCTCT GGAGC...AGCGC GTTTGATGAG TCAGGCGCTG CGTAAGATGA
<i>pseudotuberculosis</i>			
<i>Enterobacter</i>	CTGGAAATCT	GTGATGGCTT	GACCCGTTCA GGCGC...AGCTC GTATGATGAG CCAGGCGATG CGTAAGCTTG
<i>agglomerans</i>			
<i>Enterococcus</i>	TTAGAGATTG	CCGATGCCTT	AGTTTCAAGT GGTC...AGCTC GACTAATGTC TCAAGCACTA CGTAAATTAT
20 <i>faecium</i>			
<i>Escherichia</i>	CTGGAAATCT	GTGACGCCCT	GGCGCGTTCT GGCGC...GGCAC GTATGATGAG CCAGGCGATG CGTAAGCTTG
<i>coli</i>			

- 62 -

Haemophilus influenzae	GC <u>GAACAGAA</u> <u>GAATAGAATT</u> <u>TTAATGCATT</u> <u>ACCGC...</u> <u>GACCT</u> <u>GTGAGTTTAC</u> <u>GCAAAGCTTG</u> <u>AGACATTAAA</u>
Helicobacter pylori	TTAGAAATTT TAGAAAGGAT CACCAGAAGC GGAGG...AGCAA GGCTTATGAG CCATGCGTTA AGAAAAATCA
5 Lactococcus lactis	CTTCAAATTG CTGAAAATT GATTACTTCT GGAGC...AGCAC GTATGATGTC ACAAGCCATG CGTAAACTTG
Legionella pneumophila	CTGGAAATTA CTGATATGCT GGTGCGTTCT GCAGC...GGCAA GATTGATGTC GCAAGCCCTG CGTAAATTGA
Mycoplasma	TTTGCTCTTA TCGAATCATT AATTAAACA AACAA...TGCAA GATTGATGTC AAAAGGTTG CGAAGAATAC
10 genitalium	TTGGAAATCT GCGACAGCT CGTCCGTTCT GGCGG...GGCGC GCGTATGAG TCAGGCTTG CGCAAACTGA
Neisseria gonorrhoeae	CTGGAAATTT GTGATGCATT ATCTCGCTCT GTTGC...CGCAC GTATGATGAG CCAAGCTATG CGTAAACTAG
Proteus mirabilis	CTGGAAATCA CCGACATGCT GGTGCGCTCC AACGC...GGCAC GCGTATGATGTC CCAGGCGCTG CGCAAGATCA
15 Pseudomonas aeruginosa	CTGGAAATCT GTGATGCGCT GACCCGCTCC GGCGC...GGCGC GCATGATGAG CCAGGCGATG CGTAAAGCTGG
Serratia marcescens	CTGGAAATCT GTGACGCCCT GCGCGCTTCT GGCGC...GGCAC GTATGATGAG CCAGGCGATG CGTAAAGCTGG
Shigella flexneri	CTTGAAATCG CCGAAGCATT TGTAGAAGT GTTGC...AGCTC GTTTAATGTC ACAAGCGTTA CGTAAACTTT
20 Staphylococcus aureus	TTAGAAATTG CAGGAAATT GATTGACTCT GGGGC..... 32
Streptococcus gordonii	CTTGAAATTG CAGGGAATT GATTGATTCT GGCGC...AGCAC GCATGATGAG TCAAGCGATG CGTAAATTAT 33
25 Streptococcus mutans	

Streptococcus CTTGAGATTG CGGGAATAAT GATTGACTCA GGTGC...GGCTC GTATGATGAG CCAGGCCATG CGTAAACTTG 34
pneumoniae
Streptococcus CTTGAAATTG CAGGTAAATT GATTGATTCT GGTGC...AGCAC GTATGATGAG TCAGGCCATG CGTAAATTAT 35
pyogenes
5 Streptococcus CTCGAAATTG CAGGTAAGCT GATTGACTCT GGTGC...AGCGC GTATGATGAG TCAAGGCCATG CGTAAACTTT 36
salivarius
Vibrio CTGGAATAAT GTGATGCACT GGCTCGCTCT GGTGC...AGCGC GTATGTTGTC GCAAGCAATG CGTAAACTGA
cholerae
Yersinia CTGGAATAAT GTGATGCGCT GACTCGCTCT GGTGC...CGCGC GTATGATGAG CCAGGCTATG CGTAAAGCTGG
10 pestis
Selected GAAATTG CAGGIAAATT GATTGA ATGATGAG TCAIGCCATG CGTAA
sequences^a
Selected SEQ ID NO: 21 SEQ ID NO: 22^b
15 genus-specific
primer GAAATTG CAGGIAAATT GATTGA TTACGCAT GGCITGACTC ATCAT
sequences^a:

The sequence numbering refers to the *S.pneumoniae* *recA* sequence. Underlined nucleotides are identical to the selected sequence or match that sequence.

^a "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.
^b This sequence is the reverse complement of the above *recA* sequence.

Annex VI: Specific and ubiquitous primers for DNA amplification

	SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO	Nucleotide position
5	<u>Bacterial species:</u> <i>Enterococcus faecium</i>			
	1	5'-TGC TTT AGC AAC AGC CTA TCA G	26 ^a	273-294
	2 ^b	5'-TAA ACT TCT TCC GGC ACT TCG	26 ^a	468-488
10	<u>Bacterial species:</u> <i>Listeria monocytogenes</i>			
	3	5'-TGC GGC TAT AAA TGA AGA GGC	27 ^a	339-359
	4 ^b	5'-ATC CGA TGA TGC TAT GGC TTT	27 ^a	448-468
15	<u>Bacterial species:</u> <i>Neisseria meningitidis</i>			
	5	5'-CCA GCG GTA TTG TTT GGT GGT	28 ^a	56-76
	6 ^b	5'-CAG GCG GCC TTT AAT AAT TTC	28 ^a	212-232
20	<u>Bacterial species:</u> <i>Staphylococcus saprophyticus</i>			
	7	5'- AGA TCG AAT TCC ACA TGA AGG TTA TTA TGA	29 ^c	290-319
	8 ^b	5'- TCG CTT CTC CCT CAA CAA TCA AAC TAT CCT	29 ^c	409-438
25	<u>Bacterial species:</u> <i>Streptococcus agalactiae</i>			
	9	5'-TTT CAC CAG CTG TAT TAG AAG TA	30 ^a	59-81
	10 ^b	5'-GTT CCC TGA ACA TTA TCT TTG AT	30 ^a	190-212
30	<u>Fungal species:</u> <i>Candida albicans</i>			
	11	5'-CAA GAA GGT TGG TTA CAA CCC AAA GA	120 ^c	61-86
	12 ^b	5'-AGG TCT TAC CAG TAA CTT TAC CGG AT	120 ^c	184-209

^a Sequences from databases.

35 ^b These sequences are from the opposite DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c Sequences determined by our group.

Annex VI: Specific and ubiquitous primers for DNA amplification
(continues on next page)

	SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO	Nucleotide position
5	<u>Bacterial genus: <i>Enterococcus</i></u>			
	13	5'-TAC TGA CAA ACC ATT CAT GAT G	131-134 ^{a,b}	319-340 ^c
	14 ^d	5'-AAC TTC GTC ACC AAC GCG AAC	131-134 ^{a,b}	410-430 ^c
10	<u>Bacterial genus: <i>Neisseria</i></u>			
	15	5'-CTG GCG CGG TAT GGT CGG TT	31 ^e	21-40 ^f
	16 ^d	5'-GCC GAC GTT GGA AGT GGT AAA G	31 ^e	102-123 ^f
	<u>Bacterial genus: <i>Staphylococcus</i></u>			
15	17	5'-CCG TGT TGA ACG TGG TCA AAT CAA A	140-143 ^{a,b}	391-415 ^g
	18 ^d	5'-TRT GTG GTG TRA TWG WRC CAG GAG C	140-143 ^{a,b}	584-608 ^g
	19	5'-ACA ACG TGG WCA AGT WTT AGC WGC T	140-143 ^{a,b}	562-583 ^g
	20 ^d	5'-ACC ATT TCW GTA CCT TCT GGT AAG T	140-143 ^{a,b}	729-753 ^g
20	<u>Bacterial genus: <i>Streptococcus</i></u>			
	21	5'-GAA ATT GCA GGI AAA TTG ATT GA	32-36 ^e	418-440 ^h
	22 ^d	5'-TTA CGC ATG GCI TGA CTC ATC AT	32-36 ^e	547-569 ^h
25	Universal primers			
	23	5'-ACI KKI ACI GGI GTI GAR ARG TT	118-146 ^{a,b} 147-171 ^{a,e}	493-515 ⁱ
	24 ^d	5'-AYR TTI TCI CCI GGC ATI ACC AT	118-146 ^{a,b} 147-171 ^{a,e}	778-800 ⁱ

30 ^a These sequences were aligned to derive the corresponding primer.

^b *tuf* sequences determined by our group.

^c The nucleotide positions refer to the *E. faecalis tuf* gene fragment (SEQ ID NO: 132).

35 ^d These sequences are from the opposite DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^e Sequences from databases.

^f The nucleotide positions refer to the *N. meningitidis asd* gene fragment (SEQ ID NO: 31).

- ^g The nucleotide positions refer to the *S. aureus tuf* gene fragment (SEQ ID NO: 140).
- ^h The nucleotide positions refer to the *S. pneumoniae recA* gene (SEQ ID NO: 34).
- 5 ⁱ The nucleotide positions refer to the *E. coli tuf* gene fragment (SEQ ID NO: 154).

Annex VI: Specific and ubiquitous primers for DNA amplification

SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO	Nucleotide position
<u>Antibiotic resistance gene: bla_{tem}</u>			
5	37 5'-CTA TGT GGC GCG GTA TTA TC	-	-
	38 5'-CGC AGT GTT ATC ACT CAT GG	-	-
	39 5'-CTG AAT GAA GCC ATA CCA AA	-	-
	40 5'-ATC AGC AAT AAA CCA GCC AG	-	-
<u>Antibiotic resistance gene: bla_{shv}</u>			
10	41 5'-TTA CCA TGA GCG ATA ACA GC	-	-
	42 5'-CTC ATT CAG TTC CGT TTC CC	-	-
	43 5'-CAG CTG CTG CAG TGG ATG GT	-	-
	44 5'-CGC TCT GCT TTG TTA TTC GG	-	-
<u>Antibiotic resistance gene: bla_{rob}</u>			
20	45 5'-TAC GCC AAC ATC GTG GAA AG	-	-
	46 5'-TTG AAT TTG GCT TCT TCG GT	-	-
	47 5'-GGG ATA CAG AAA CGG GAC AT	-	-
	48 5'-TAA ATC TTT TTC AGG CAG CG	-	-
<u>Antibiotic resistance gene: bla_{oxa}</u>			
30	49 5'-GAT GGT TTG AAG GGT TTA TTA TAA G	110 ^a	686-710
	50 ^b 5'-AAT TTA GTG TGT TTA GAA TGG TGA T	110 ^a	802-826
<u>Antibiotic resistance gene: bla_Z</u>			
35	51 5'-ACT TCA ACA CCT GCT GCT TTC	111 ^a	511-531
	52 ^b 5'-TGA CCA CTT TTA TCA GCA ACC	111 ^a	663-683
<u>Antibiotic resistance gene: aadB</u>			
40	53 5'-GGC AAT AGT TGA AAT GCT CG	-	-
	54 5'-CAG CTG TTA CAA CGG ACT GG	-	-
<u>Antibiotic resistance gene: aacC1</u>			
45	55 5'-TCT ATG ATC TCG CAG TCT CC	-	-
	56 5'-ATC GTC ACC GTA ATC TGC TT	-	-

^a Sequences from databases.^b These sequences are from the opposite DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex VI: Specific and ubiquitous primers for DNA amplification

	SEQ ID NO	Nucleotide sequence	Originating DNA fragment		
			SEQ ID NO	Nucleotide position	
5	<u>Antibiotic resistance gene: aacC2</u>				
	57	5'-CAT TCT CGA TTG CTT TGC TA	-	-	
	58	5'-CCG AAA TGC TTC TCA AGA TA	-	-	
10	<u>Antibiotic resistance gene: aacC3</u>				
	59	5'-CTG GAT TAT GGC TAC GGA GT	-	-	
	60	5'-AGC AGT GTG ATG GTA TCC AG	-	-	
15	<u>Antibiotic resistance gene: aac6'-IIa</u>				
	61	5'-GAC TCT TGA TGA AGT GCT GG	112 ^a	123-142	
	62 ^b	5'-CTG GTC TAT TCC TCG CAC TC	112 ^a	284-303	
20	63	5'-TAT GAG AAG GCA GGA TTC GT	112 ^a	445-464	
	64 ^b	5'-GCT TTC TCT CGA AGG CTT GT	112 ^a	522-541	
	<u>Antibiotic resistance gene: aacA4</u>				
25	65	5'-GAG TTG CTG TTC AAT GAT CC	-	-	
	66	5'-GTG TTT GAA CCA TGT ACA CG	-	-	
	<u>Antibiotic resistance gene: aad(6')</u>				
30	173	5'-TCT TTA GCA GAA CAG GAT GAA	-	-	
	174	5'-GAA TAA TTC ATA TCC TCC G	-	-	
	<u>Antibiotic resistance gene: vanA</u>				
35	67	5'-TGT AGA GGT CTA GCC CGT GT	-	-	
	68	5'-ACG GGG ATA ACG ACT GTA TG	-	-	
	69	5'-ATA AAG ATG ATA GGC CGG TG	-	-	
	70	5'-TGC TGT CAT ATT GTC TTG CC	-	-	
40	<u>Antibiotic resistance gene: vanB</u>				
	71	5'-ATT ATC TTC GGC GGT TGC TC	116 ^a	22-41	
	72 ^b	5'-GAC TAT CGG CTT CCC ATT CC	116 ^a	171-190	
45	73	5'-CGA TAG AAG CAG CAG GAC AA	116 ^a	575-594	
	74 ^b	5'-CTG ATG GAT GCG GAA GAT AC	116 ^a	713-732	

^a Sequences from databases.^b These sequences are from the opposite DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex VI: Specific and ubiquitous primers for DNA amplification

SEQ ID NO	Nucleotide sequence	Originating DNA fragment		
		SEQ ID NO	Nucleotide position	
5	<u>Antibiotic resistance gene: <i>vanC</i></u>			
75	5'-GCC TTA TGT ATG AAC AAA TGG	117 ^a	373-393	
76 ^b	5'-GTG ACT TTW GTG ATC CCT TTT GA	117 ^a	541-563	
10	<u>Antibiotic resistance gene: <i>msrA</i></u>			
77	5'-TCC AAT CAT TGC ACA AAA TC	-	-	
78	5'-AAT TCC CTC TAT TTG GTG GT	-	-	
15	79	5'-TCC CAA GCC AGT AAA GCT AA	-	-
80	5'-TGG TTT TTC AAC TTC TTC CA	-	-	
20	<u>Antibiotic resistance gene: <i>sata</i></u>			
81	5'-TCA TAG AAT GGA TGG CTC AA	-	-	
82	5'-AGC TAC TAT TGC ACC ATC CC	-	-	
25	<u>Antibiotic resistance gene: <i>aac(6')-aph(2'')</i></u>			
83	5'-CAA TAA GGG CAT ACC AAA AAT C	-	-	
84	5'-CCT TAA CAT TTG TGG CAT TAT C	-	-	
85	5'-TTG GGA AGA TGA AGT TTT TAG A	-	-	
86	5'-CCT TTA CTC CAA TAA TTT GGC T	-	-	
30	<u>Antibiotic resistance gene: <i>vat</i></u>			
87	5'-TTT CAT CTA TTC AGG ATG GG	-	-	
88	5'-GGA GCA ACA TTC TTT GTG AC	-	-	
35	<u>Antibiotic resistance gene: <i>vga</i></u>			
89	5'-TGT GCC TGA AGA AGG TAT TG	-	-	
90	5'-CGT GTT ACT TCA CCA CCA CT	-	-	
40	<u>Antibiotic resistance gene: <i>ermA</i></u>			
91	5'-TAT CTT ATC GTT GAG AAG GGA TT	113 ^a	370-392	
92 ^b	5'-CTA CAC TTG GCT TAG GAT GAA A	113 ^a	487-508	

45 ^a Sequences from databases.

^b These sequences are from the opposite DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex VI: Specific and ubiquitous primers for DNA amplification

SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO	Nucleotide position
<u>Antibiotic resistance gene: <i>ermB</i></u>			
5	93 5'-CTA TCT GAT TGT TGA AGA AGG ATT	114 ^a	366-389
	94 ^b 5'-GTT TAC TCT TGG TTT AGG ATG AAA	114 ^a	484-507
<u>Antibiotic resistance gene: <i>ermC</i></u>			
10	95 5'-CTT GTT GAT CAC GAT AAT TTC C	115 ^a	214-235
	96 ^b 5'-ATC TTT TAG CAA ACC CGT ATT C	115 ^a	382-403
<u>Antibiotic resistance gene: <i>mecA</i></u>			
15	97 5'-AAC AGG TGA ATT ATT AGC ACT TGT AAG	-	-
	98 5'-ATT GCT GTT AAT ATT TTT TGA GTT GAA	-	-
<u>Antibiotic resistance gene: <i>int</i></u>			
20	99 5'-GTG ATC GAA ATC CAG ATC C	-	-
	100 5'-ATC CTC GGT TTT CTG GAA G	-	-
25	101 5'-CTG GTC ATA CAT GTG ATG G	-	-
	102 5'-GAT GTT ACC CGA GAG CTT G	-	-
<u>Antibiotic resistance gene: <i>sul</i></u>			
30	103 5'-TTA AGC GTG CAT AAT AAG CC	-	-
	104 5'-TTG CGA TTA CTT CGC CAA CT	-	-
	105 5'-TTT ACT AAG CTT GCC CCT TC	-	-
	106 5'-AAA AGG CAG CAA TTA TGA GC	-	-

35 ^a Sequences from databases.

^b These sequences are from the opposite DNA strand of the sequence of the originating fragment given in the Sequence Listing.

- 71 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: INFECTIO DIAGNOSTIC (I.D.I.) INC.
(B) STREET: 2050, BOULEVARD RENE LEVESQUE OUEST, 4E ETAGE
(C) CITY: STE-FOY
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) POSTAL CODE (ZIP): G1V 2K8
(G) TELEPHONE: (418) 681-4343
(H) TELEFAX: (418) 681-5254

(A) NAME: BERGERON, MICHEL G.
(B) STREET: 2069 RUE BRULARD
(C) CITY: SILLERY
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) POSTAL CODE (ZIP): G1T 1G2

(A) NAME: PICARD, FRANCOIS J.
(B) STREET: 1245, RUE DE LA SAPINIERE
(C) CITY: CAP-ROUGE
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) POSTAL CODE (ZIP): G1Y 1A1

(A) NAME: OUELLETTE, MARC
(B) STREET: 1035 DE PLOERMEL
(C) CITY: SILLERY
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) POSTAL CODE (ZIP): G1S 3S1

(A) NAME: ROY, PAUL H.
(B) STREET: 28, RUE CHARLES GARNIER
(C) CITY: LORETTEVILLE
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) POSTAL CODE (ZIP): G2A 3S1

(ii) TITLE OF INVENTION: SPECIES-SPECIFIC, GENIUS-SPECIFIC AND
UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY
DETECT AND IDENTIFY COMMON BACTERIAL AND FUNGAL PATHOGENS
AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES ...

(iii) NUMBER OF SEQUENCES: 174

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

- 72 -

- (A) APPLICATION NUMBER: US 08/743,637
(B) FILING DATE: 04-NOV-1996

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecium*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TGCTTTAGCA ACAGCCTATC AG

22

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecium*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TAAACTTCTT CCGGCACTTC G

21

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Listeria monocytogenes*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGCGGCTATA AATGAAGAGG C

21

(2) INFORMATION FOR SEQ ID NO: 4:

- 73 -

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATCCGATGAT GCTATGGCTT T

21

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCAGCGGTAT TGTTTGGTGG T

21

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CAGGCGGCCT TTAATAATTT C

21

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- 74 -

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AGATCGAATT CCACATGAAG GTTATTATGA

30

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TCGCTTCTCC CTCAACAATC AAACATATCT

30

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTTCACCAGC TGTATTAGAA GTA

23

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus agalactiae*

- 75 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GTTCCCTGAA CATTATCTTT GAT

23

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CAAGAAGGTT GGTTACAACC CAAAGA

26

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AGGTCTTACC AGTAACTTTA CCGGAT

26

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TACTGACAAA CCATTCATGA TG

22

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

- 76 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AACTTCGTCA CCAACGCGAA C

21

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTGGCGCGGT ATGGTCGGTT

20

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GCCGACGTTG GAAGTGGTAA AG

22

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CCGTGTTGAA CGTGGTCAAA TCAAA

25

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs

- 77 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TRTGTGGTGT RATWGWCCA GGAGC

25

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ACAACGTGGW CAAGTWTAG CWGCT

25

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ACCATTTCWG TACCTTCTGG TAAGT

25

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GAAATTGCAG GNAAATTGAT TGA

23

- 78 -

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TTACGCATGG CNTGACTCAT CAT

23

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:3
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:9
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:15
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

- 79 -

ACNKKNACNG GNGTNGARAT GTT

23

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:6
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:9
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:12
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:18
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

AYRTTNTCNC CNGGCATNAC CAT

23

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TCGCTTCTCC

10

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 600 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- 80 -

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TTCTTAGAGA CATTGAATAT GCCTTATGTC GGCGCAGGCG TATTGACCAG TGCATGTGCC	60
ATGGATAAAA TCATGACCAA GTATATTTTA CAAGCTGCTG GTGTGCCGCA AGTTCCTTAT	120
GTACCAGTAC TTAAGAATCA ATGGAAAGAA AATCCTAAAA AAGTATTTGA TCAATGTGAA	180
GGTTCTTTGC TTTATCCGAT GTTTGTCAAA CCTGCGAATA TGGGTTCTAG TGTCGGCATT	240
ACAAAGGCAG AAAACCGAGA AGAGCTGCAA AATGCTTTAG CAACAGCCTA TCAGTATGAT	300
TCTCGAGCAA TCGTTGAACA AGGAATTGAA GCGCGCGAAA TCGAAGTTGC TGTATTAGGA	360
AATGAAGATG TTCGACGAC TTTGCCTGGC GAAGTCGTAA AAGACGTAGC ATTCTATGAT	420
TATGAAGCCA AATATATCAA TAATAAAATC GAAATGCAGA TTCCAGCCGA AGTGCCGGAA	480
GAAGTTTATC AAAAAGCGCA AGAGTACGCG AAGTTAGCTT ACACGATGTT AGGTGGAAGC	540
GGATTGAGCC GGTGCGATTT CTTTTTGACA AATAAAAATG AATTATTCCT GAATGAATTA	600

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1920 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GTGGGATTAA ACAGATTTAT GCGTGCGATG ATGGTGGTTT TCATTACTGC CAATTGCATT	60
ACGATTAACC CCGACATAAT ATTTGCAGCG ACAGATAGCG AAGATTCTAG TCTAAACACA	120
GATGAATGGG AAGAAGAAAA AACAGAAGAG CAACCAAGCG AGGTAAATAC GGGACCAAGA	180
TACGAAACTG CACGTGAAGT AAGTTCACGT GATATTAAAG AACTAGAAAA ATCGAATAAA	240
GTGAGAAATA CGAACAAAGC AGACCTAATA GCAATGTTGA AAGAAAAAGC AGAAAAAGGT	300
CCAAATATCA ATAATAACAA CAGTGAACAA ACTGAGAATG CGGCTATAAA TGAAGAGGCT	360

- 81 -

TCAGGAGCCG	ACCGACCAGC	TATACAAGTG	GAGCGTCGTC	ATCCAGGATT	GCCATCGGAT	420
AGCGCAGCGG	AAATTAAAAA	AAGAAGGAAA	GCCATAGCAT	CATCGGATAG	TGAGCTTGAA	480
AGCCTTACTT	ATCCGGATAA	ACCAACAAAA	GTAAATAAGA	AAAAAGTGGC	GAAAGAGTCA	540
GTTGCGGATG	CTTCTGAAAG	TGACTTAGAT	TCTAGCATGC	AGTCAGCAGA	TGAGTCTTCA	600
CCACAACCTT	TAAAAGCAAA	CCAACAACCA	TTTTTCCCTA	AAGTATTTAA	AAAAATAAAA	660
GATGCGGGGA	AATGGGTACG	TGATAAAATC	GACGAAAATC	CTGAAGTAAA	GAAAGCGATT	720
GTTGATAAAA	GTGCAGGGTT	AATTGACCAA	TTATTAACCA	AAAAGAAAAG	TGAAGAGGTA	780
AATGCTTCGG	ACTTCCCGCC	ACCACCTACG	GATGAAGAGT	TAAGACTTGC	TTTGCCAGAG	840
ACACCAATGC	TTCTTGTTTT	TAATGCTCCT	GCTACATCAG	AACCGAGCTC	ATTCGAATTT	900
CCACCACCAC	CTACGGATGA	AGAGTTAAGA	CTTGCTTTGC	CAGAGACGCC	AATGCTTCTT	960
GGTTTTAATG	CTCCTGCTAC	ATCGGAACCG	AGCTCGTTTCG	AATTTCCACC	GCCTCCAACA	1020
GAAGATGAAC	TAGAAATCAT	CCGGGAAACA	GCATCCTCGC	TAGATTCTAG	TTTTACAAGA	1080
GGGGATTTAG	CTAGTTTGAG	AAATGCTATT	AATCGCCATA	GTCAAATTTT	CTCTGATTTT	1140
CCACCAATCC	CAACAGAAGA	AGAGTTGAAC	GGGAGAGGCG	GTAGACCAAC	ATCTGAAGAA	1200
TTTAGTTCGC	TGAATAGTGG	TGATTTTACA	GATGACGAAA	ACAGCGAGAC	AACAGAAGAA	1260
GAAATTGATC	GCCTAGCTGA	TTTAAGAGAT	AGAGGAACAG	GAAAACACTC	AAGAAATGCG	1320
GGTTTTTTTAC	CATTAAATCC	GTTTGCTAGC	AGCCCGGTTT	CTTCGTTAAG	TCCAAAGGTA	1380
TCGAAAATAA	GCGACCGGGC	TCTGATAAGT	GACATAACTA	AAAAAACGCC	ATTTAAGAAT	1440
CCATCACAGC	CATTAAATGT	GTTTAATAAA	AAACTACAA	CGAAAACAGT	GAATAAAAAA	1500
CCAACCCCTG	TAAAGACCGC	ACCAAAGCTA	GCAGAACTTC	CTGCCACAAA	ACCACAAGAA	1560
ACCGTACTTA	GGGAAAATAA	AACACCCCTT	ATAGAAAAAC	AAGCAGAAAC	AAACAAGCAG	1620
TCAATTAATA	TGCCGAGCCT	ACCAGTAATC	CAAAAAGAAG	CTACAGAGAG	CGATAAAGAG	1680
GAAATGAAAC	CACAAACCGA	GGAAAAAATG	GTAGAGGAAA	GCGAATCAGC	TAATAACGCA	1740
AACGGAAAAA	ATCGTTCTGC	TGGCATTGAA	GAAGGAAAAA	TAATTGCTAA	AAGTGCAGAA	1800
GACGAAAAAG	CGAAGGAAGA	ACCAGGGAAC	CATACGACGT	TAATTCTTGC	AATGTTAGCT	1860
ATTGGCGTGT	TCTCTTTAGG	GGCGTTTATC	AAAATTATTC	AATTAAGAAA	AAATAATTAA	1920

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 415 base pairs

- 82 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TACCGGTACG CTAAATATTG GTGATGTATT GGATATTATG ATTTGGGAAG CGCCGCCAGC	60
GGTATTGTTT GGTGGTGGCC TTTCTTCGAT GGGCTCGGGT AGTGCGCAAC AAACCAAGTT	120
GCCGGAGCAA CTGGTGACGG CACGTGGTAC GGTTTCTGTG CCGTTTGTGTG GCGATATTTT	180
GGTGGTTCGGT AAAACGCCTG GTCAGGTTCA GGAAATTATT AAAGGCCGCC TGAAAAAAT	240
GGCCAATCAG CCGCAAGTGA TGGTGCGCTT GGTGCAGAAT AATGCGGCAA ATGTATCGGT	300
GATTCGCGCA GGCAATAGTG TCGTATGCC GTTGACGGCA GCCGGTGAGC GTGTGTTGGA	360
TGCGGTGGCT GCGGTAGGTG GTTCAACGGC AAATGTGCAG GATACGAATG TGCAG	415

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TCGCTTCTCC AGAAGAAATT TTAGAAACAT ATCTAGAAAA TCCCAAATTA GATAAACCGT	60
TTATATTATG TGAATACGCA CATGCAATGG GAAATTCACC AGGAGATCTT AATGCATATC	120
AAACATTAAT TGAAAAATAT GATAGTTTTA TTGGCGGTTT TGTTTGGGAA TGGTGTGATC	180
ATAGCATTCA GGTGCGGATA AAGGAAGGTA AACCAATTTT TAGATATGGT GGAGATTTTG	240
GTGAGGCCTT ACATGACGGT AATTTTGTG TTGATGGTAT TGTTTCGCCA GATCGAATTC	300
CACATGAAGG TTATTATGAG TTAAACATG AACATAGACC TTTGAGATTG GTTAACGAAG	360
AGGATTATCG GTTTACATTG AAGAATCAAT TTGATTTTAC AAATGCGGAG GATAGTTTGA	420
TTGTTGAGGG AGAAGCGA	438

- 83 -

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

ATGAACGTTA CACATATGAT GTATCTATCT GGAACTCTAG TGGCTGGTGC ATTGTTATTT	60
TCACCAGCTG TATTAGAAGT ACATGCTGAT CAAGTGACAA CTCCACAAGT GGTAATCAT	120
GTAAATAGTA ATAATCAAGC CCAGCAAATG GCTCAAAAGC TTGATCAAGA TAGCATTCAG	180
TTGAGAAATA TCAAAGATAA TGTTCAAGGA ACAGATTATG AAAAACCGGT TAATGAGGCT	240
ATTACTAGCG TGGAAAAATT AAAGACTTCA TTGCGTGCCA ACCCTGAGAC AGTTTATGAT	300
TTGAATTCTA TTGGTAGTCG TGTAGAAGCC TTAACAGATG TGATTGAAGC AATCACTTTT	360
TCAACTCAAC ATTTAACAAA TAAGGTTAGT CAAGCAAATA TTGATATGGG ATTTGGGATA	420
ACTAAGCTAG TTATTCGCAT TTTAGATCCA TTTGCTTCAG TTGATTCAAT TAAAGCTCAA	480
GTTAACGATG TAAAGGCATT AGAACAAAAA GTTTTAACTT ATCCTGATTT AAAACCAACT	540
GATAGAGCTA CCATCTATAC AAAATCAAAA CTTGATAAGG AAATCTGGAA TACACGCTTT	600
ACTAGAGATA AAAAAGTACT TAACGTCAAA GAATTTAAAG TTTACAATAC TTAAATAAA	660
GCAATCACAC ATGCTGTTGG AGTTCAGTTG AATCCAAATG TTACGGTACA ACAAGTTGAT	720
CAAGAGATTG TAACATTACA AGCAGCACTT CAAACAGCAT TAAAATAA	768

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

- 84 -

```

ATGAAAGTAG GTTTCGTCGG CTGGCGCGGT ATGGTCGGTT CGGTTTTGAT GCAGCGTATG      60
AAAGAAGAAA ACGACTTCGC CCACATTCCC GAAGCGTTTT TCTTTACCAC TTCCAACGTC      120
GGCGGCGCAC GCCCTGATTT CGGTCAGGCG GCTAAAACAT TATTGGACGC GAACAACGTT      180
GCCGAGCTGG CAAAAATGGA CATCATCGTT ACCTGCCAAG GCGGCGACTA CACCAAATCC      240
GTCTTCCAAG CCCTGCGCGA CAGCGGCTGG AACGGCTACT GGATTGACGC GGCATCCTCG      300
CTGCGTATGA AAGACGACGC GATTATCGTC CTCGACCCCG TCAACCGCAA CGTCATCGAC      360
AACGGCCTCA AAAACGGCGT GAAAAACTAC ATCGGCGGCA ACTGTACCGT TTCCCTGATG      420
C                                          421

```

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

TTCATAGACG CTGAGCACGC TTTGGATCCA TCTTACGCGG CTGCTCTAGG TGTAATATT      60
GATGAGCTGT TGCTATCTCA ACCAGATTCT GGTGAGCAAG GTTTAGAAAT TGCAGGAAAA      120
TTGATTGACT CTGGGGCAGT TGATTTAGTT GTCATCGACT CTGTTGCAGC TCTTGTACCA      180
CGTGCGGAAA TCGATGGAGA TATCGGTGAT AGC                                          213

```

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```

GGGCCGGAAT CTTCTGGTAA GACAACTGTC GCTCTTCATG CTGCTGCTCA GGCGCAAAAA      60

```

- 85 -

GATGGCGGTA TTGCCGCTTT CATTGATGCA GAACATGCCC TTGATCCAGC CTATGCTGCT	120
GCTCTTGGCG TTAATATTGA TGAGCTTTTG CTTTCACAAC CAGATTCAGG AGAACAGGGT	180
CTTGAAATTG CAGGGAAATT GATTGATTCT GGCGCTGTTG ATTTAGTTGT TGTGACTCA	240
GTGGCAGCTT TAGTACCACG TCGGAGATT GACGGAGATA TTGGTAATAG TCATGTTGGC	300
TTACAAGCAC GCATGATGAG TCAAGCGATG CGTAAATTAT CAGCTTCAAT CAATAAAACA	360
AAAACCATTG CTATTTTAT TAATCAATTG CGGGAAAAAG TTGGTATTAT GTTTGGTAAT	420
CCAGAAACAA CCCCTGGCGG GCGTGCCTTG AAGTTTTATT CTTCTGTGCG TCTTGATGTC	480
CGCGGCAATA CTCAAATTAA AGGAACCGGG GAACAAAAAG ACAGCAATAT TGGTAAAGAG	540
ACCAAAATTA AAGTTGTTAA AAATAAAGTT GCTCCACCAT TTAAGGAAGC TTTTGTAGAA	600
ATTATATATG GTGAAGGCAT TTCTCGTACA GGTGAATTAG TTAAGATTGC CAGTGATTTG	660
GGAATTATCC AAAAAGCTGG AGCTTGGTAC TC	692

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

ATGGCGAAAA AACCAAAAAA ATTAGAAGAA ATTTCAAAAA AATTTGGGGC AGAACGTGAA	60
AAGGCCTTGA ATGACGCTCT TAAATTGATT GAGAAAGACT TTGGTAAAGG ATCAATCATG	120
CGTTTGGGTG AACGTGCGGA GCAAAAGGTG CAAGTGATGA GCTCAGGTTT TTTAGCTCTT	180
GACATTGCCC TTGGCTCAGG TGGTTATCCT AAGGGACGTA TCATCGAAAT CTATGGCCCA	240
GAGTCATCTG GTAAGACAAC GGTGCCCCTT CATGCAGTTG CACAAGCGCA AAAAGAAGGT	300
GGGATTGCTG CCTTTATCGA TCGGGAACAT GCCCTTGATC CAGCTTATGC TGCGGCCCTT	360
GGTGTCAATA TTGACGAATT GCTCTGTCT CAACCAGACT CAGGAGAGCA AGGTCTTGAG	420
ATTGCGGGAA AATTGATTGA CTCAGGTGCA GTTGATCTTG TCGTAGTCGA CTCAGTTGCT	480
GCCCTTGTTT CTCGTGCGGA AATTGATGGA GATATCGGAG ATAGCCATGT TGGTTTGCAG	540
GCTCGTATGA TGAGCCAGGC CATGCGTAAA CTTGGCGCCT CTATCAATAA AACCAAAACA	600

- 86 -

ATTGCCATTT TTATCAACCA ATTGCGTGAA AAAGTTGGAG TGATGTTTGG AAATCCAGAA	660
ACAACACCGG GCGGACGTGC TTTGAAATTC TATGCTTCAG TCCGCTTGGA TGTTCGTGGT	720
AATACACAAA TTAAGGGAAC TGGTGATCAA AAAGAAACCA ATGTCGGTAA AGAAACTAAG	780
ATTAAGGTTG TAAAAAATAA GGTAGCTCCA CCGTTTAAGG AAGCCGTAGT TGAAATTATG	840
TACGGAGAAG GAATTTCTAA GACTGGTGAG CTTTTGAAGA TTGCAAGCGA TTTGGATATT	900
ATCAAAAAAG CAGGGGCTTG GTATTCTTAC AAAGATGAAA AAATTGGGCA AGGTTCTGAG	960
AATGCTAAGA AATACTTGGC AGAGCACCCA GAAATCTTTG ATGAAATTGA TAAGCAAGTC	1020
CGTTCTAAAT TTGGCTTGAT TGATGGAGAA GAAGTTTCAG AACAAGATAC TGAAAACAAA	1080
AAAGATGAGC CAAAGAAAGA AGAAGCAGTG AATGAAGAAG TTCCGCTTGA CTTAGGCGAT	1140
GAAGTTGAAA TCGAAATTGA AGAATAAGCT GTTAAAGCAG TGGAGAAATC CGCTACTTTT	1200
TCGA	1204

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATGCGTTCAG GAAGTCTAGC TCTTGATATT GCTTGGATAG CTGGTGGTTA TCCTAAAGGA	60
CGTATCATCG AAATCTATGG TCCAGAGTCT TCCGGTAAAA CGACTGTGGC TTTACATGCT	120
GTAGCACAAG CTCAAAAAGA AGGTGGAATC GCAGCCTTTA TCGATGCCGA GCATGCGCTT	180
GATCCAGCTT ATGCTGCTGC GCTTGGGGTT AATATTGATG AACTTCTCTT GTCTCAACCA	240
GATTCTGGAG AACAAGGACT TGAAATTGCA GGTAAATTGA TTGATTCTGG TGCGGTTGAC	300
CTGGTTGTTG TCGATTCACT AGCAGCTTTA GTGCCACGTG CTGAAATTGA TGGTGATATT	360
GGCGATAGCC ATGTCGGATT GCAAGCACGT ATGATGAGTC AGGCCATGCG TAAATTATCA	420
GCTTCTATTA ATAAAACAAA AACTATCGCA ATCTTTATCA ACCAATTGCG TGAAAAAGTT	480
GGTGTGATGT TTGGAAATCC TGAAACAACA CCAGGTGGTC GAGCTTTGAA ATTCTATGCT	540
TCTGTTCCGC TGGATGTGCG TGGAAACAAC CAAATTAAAG GAACTGGTGA CCAAAAGATA	600

- 87 -

```

GCCAGCATTG GTAAGGAGAC CAAAATCAAG GTTGTTAAAA ACAAGGTCGC TCCGCCATTT      660
AAGGTAGCAG AAGTTGAAAT CATGTATGGG GAAGGTATTT CTCGTACAGG GGAGCTTGTT      720
AAAATTGCTT CTGATTGGA CATTATCCAA AAAGCAGGTG CTTGGTTCTC TTATAATGGT      780
GAGAAGATTG GCCAAGGTTT TGAAAATGCT AAGCGTTATT TGGCCGATCA TCCACAATTG      840
TTTGATGAAA TCGACCGTAA AGTACGTGTT AAATTTGGTT TGCTTGAAGA AAGCGAAGAA      900
GAATCTGCTA TGGCAGTAGC ATCAGAAGAA ACCGATGATC TTGCTTTAGA TTTAGATAAT      960
GGTATTGAAA TTGAAGATTA A                                          981

```

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

GCGTATGCAC GAGCTCTAGG TGTTAATATC GATGAGCTTC TTTTGTCGCA GCCTGATTCT      60
GGTGAGCAAG GTCTCGAAAT TGCAGGTAAG CTGATTGACT CTGGTGCAGT GGATTTAGTT      120
GTTGTTGACT CAGTTGCGGC CTCGTACCA CGTGCAGAAA TTGATGGAGA TAGTGGTGAC      180
AGTCATGTAG GACTTCAAGC GCGTATGATG AGTCAAGCCA TCGGTAAACT TTCTGCATCT      240
ATTAATAAAA CAAAAACGAT TGCTATCTTT ATTAACCAGT TCGGTGAAAA AGTTGGTATC      300
ATGTTTGGTA AC                                          312

```

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```

CTATGTGGCG CGGTATTATC                                          20

```

(2) INFORMATION FOR SEQ ID NO: 38:

- 88 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CGCAGTGTTA TCACTCATGG

20

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTGAATGAAG CCATACCAA

20

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

ATCAGCAATA AACCAGCCAG

20

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

TTACCATGAG CGATAACAGC

20

(2) INFORMATION FOR SEQ ID NO: 42:

- 89 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CTCATTCAGT TCCGTTTCCC

20

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CAGCTGCTGC AGTGGATGGT

20

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

CGCTCTGCTT TGTTATTCGG

20

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

TACGCCAACA TCGTGGAAG

20

(2) INFORMATION FOR SEQ ID NO: 46:

- 90 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

TTGAATTTGG CTTCTTCGGT

20

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGGATACAGA AACGGGACAT

20

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

TAAATCTTTT TCAGGCAGCG

20

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GATGGTTTGA AGGGTTTATT ATAAG

25

(2) INFORMATION FOR SEQ ID NO: 50:

- 91 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

AATTTAGTGT GTTTAGAATG GTGAT

25

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

ACTTCAACAC CTGCTGCTTT C

21

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

TGACCACTTT TATCAGCAAC C

21

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGCAATAGTT GAAATGCTCG

20

(2) INFORMATION FOR SEQ ID NO: 54:

- 92 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

CAGCTGTTAC AACGGACTGG

20

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TCTATGATCT CGCAGTCTCC

20

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

ATCGTCACCG TAATCTGCTT

20

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CATTCTCGAT TGCTTTGCTA

20

(2) INFORMATION FOR SEQ ID NO: 58:

- 93 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CCGAAATGCT TCTCAAGATA

20

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

CTGGATTATG GCTACGGAGT

20

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

AGCAGTGTGA TGGTATCCAG

20

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACTCTTGAT GAAGTGCTGG

20

(2) INFORMATION FOR SEQ ID NO: 62:

- 94 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

CTGGTCTATT CCTCGCACTC

20

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

TATGAGAAGG CAGGATTCGT

20

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GCTTTCTCTC GAAGGCTTGT

20

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GAGTTGCTGT TCAATGATCC

20

(2) INFORMATION FOR SEQ ID NO: 66:

- 95 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GTGTTTGAAC CATGTACACG

20

(2) INFORMATION FOR SEQ ID NO: 67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TGTAGAGGTC TAGCCCGTGT

20

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

ACGGGGATAA CGACTGTATG

20

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

ATAAAGATGA TAGGCCGGTG

20

(2) INFORMATION FOR SEQ ID NO: 70:

- 96 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TGCTGTCATA TTGTCTTGCC

20

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ATTATCTTCG GCGGTTGCTC

20

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

GACTATCGGC TTCCATTCC

20

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CGATAGAAGC AGCAGGACAA

20

(2) INFORMATION FOR SEQ ID NO: 74:

- 97 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

CTGATGGATG CGGAAGATAC

20

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GCCTTATGTA TGAACAAATG G

21

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

GTGACTTTWG TGATCCCTTT TGA

23

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

TCCAATCATT GCACAAAATC

20

(2) INFORMATION FOR SEQ ID NO: 78:

- 98 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

AATTCCTCT ATTTGGTGGT

20

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TCCAAGCCA GTAAAGCTAA

20

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

TGGTTTTTCA ACTTCTTCCA

20

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

TCATAGAATG GATGGCTCAA

20

(2) INFORMATION FOR SEQ ID NO: 82:

- 99 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

AGCTACTATT GCACCATCCC

20

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CAATAAGGGC ATACCAAAAA TC

22

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

CCTTAACATT TGTGGCATT TC

22

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

TTGGGAAGAT GAAGTTTTTA GA

22

(2) INFORMATION FOR SEQ ID NO: 86:

- 100 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

CCTTTACTCC AATAATTTGG CT

22

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

TTTCATCTAT TCAGGATGGG

20

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GGAGCAACAT TCTTTGTGAC

20

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TGTGCCTGAA GAAGGTATTG

20

(2) INFORMATION FOR SEQ ID NO: 90:

- 101 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

CGTGTTACTT CACCACCACT

20

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

TATCTTATCG TTGAGAAGGG ATT

23

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CTACACTTGG CTTAGGATGA AA

22

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CTATCTGATT GTTGAAGAAG GATT

24

(2) INFORMATION FOR SEQ ID NO: 94:

- 102 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

GTTTACTCTT GGTTCAGGAT GAAA

24

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CTTGTTGATC ACGATAATTT CC

22

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

ATCTTTTAGC AAACCCGTAT TC

22

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

AACAGGTGAA TTATTAGCAC TTGTAAG

27

(2) INFORMATION FOR SEQ ID NO: 98:

- 103 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

ATTGCTGTTA ATATTTTTTTG AGTTGAA

27

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

GTGATCGAAA TCCAGATCC

19

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

ATCCTCGGTT TTCTGGAAG

19

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CTGGTCATAC ATGTGATGG

19

(2) INFORMATION FOR SEQ ID NO: 102:

- 104 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

GATGTTACCC GAGAGCTTG

19

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

TTAAGCGTGC ATAATAAGCC

20

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

TTGCGATTAC TCGCCAACT

20

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

TTTACTAAGC TTGCCCCCTTC

20

(2) INFORMATION FOR SEQ ID NO: 106:

- 105 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

AAAAGGCAGC AATTATGAGC

20

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:9
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:15
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:18
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:21
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

AAYATGATNA CNGGNGCNGC NCARATGGA

29

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid

- 106 -

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:3
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:9
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CCNACNGTNC KNCCRCCYTC RCG

23

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:15
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

- 107 -

(B) LOCATION:18

(D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CARYTNATHG TNGCNGTNAA YAARATGGA

29

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

ATGAAAAACA CAATACATAT CAACTTCGCT ATTTTTTTAA TAATTGCAAA TATTATCTAC	60
AGCAGCGCCA GTGCATCAAC AGATATCTCT ACTGTTGCAT CTCCATTATT TGAAGGAACT	120
GAAGGTTGTT TTTTACTTTA CGATGCATCC ACAAACGCTG AAATTGCTCA ATTCAATAAA	180
GCAAAGTGTG CAACGCAAAT GGCACCAGAT TCAACTTTCA AGATCGCATT ATCACTTATG	240
GCATTTGATG CGGAAATAAT AGATCAGAAA ACCATATTCA AATGGGATAA AACCCCCAAA	300
GGAATGGAGA TCTGGAACAG CAATCATACA CCAAAGACGT GGATGCAATT TTCTGTTGTT	360
TGGGTTTTCG AAGAAATAAC CCAAAAAAAT AGATTAAATA AAATCAAGAA TTATCTCAAA	420
GATTTTGATT ATGGAAATCA AGACTTCTCT GGAGATAAAG AAAGAAACAA CGGATTAACA	480
GAAGCATGGC TCGAAAGTAG CTTAAAAAAT TCACCAGAAG AACAAATTCA ATTCCTGCGT	540
AAAATTATTA ATCACAATCT CCCAGTTAAA AACTCAGCCA TAGAAAACAC CATAGAGAAC	600
ATGTATCTAC AAGATCTGGA TAATAGTACA AACTGTATG GGAAACTGG TGCAGGATTC	660
ACAGCAAATA GAACCTTACA AAACGGATGG TTTGAAGGGT TTATTATAAG CAAATCAGGA	720
CATAAATATG TTTTGTGTC CGCACTTACA GGAACTTGG GGTCGAATTT AACATCAAGC	780
ATAAAAGCCA AGAAAAATGC GATCACCATT CTAAACACAC TAAATTTATA A	831

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 108 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

TTGAAAAAGT TAATATTTTT AATTGTAATT GCTTTAGTTT TAAGTGCATG TAATTCAAAC	60
AGTTCACATG CCAAAGAGTT AAATGATTTA GAAAAAAAT ATAATGCTCA TATTGGTGT	120
TATGCTTTAG ATACTAAAAG TGGTAAGGAA GTAAATTTA ATTCAGATAA GAGATTTGCC	180
TATGCTTCAA CTTCAAAAGC GATAAATAGT GCTATTTTGT TAGAACAAGT ACCTTATAAT	240
AAGTTAAATA AAAAAGTACA TATTAACAAA GATGATATAG TTGCTTATTC TCCTATTTTA	300
GAAAAATATG TAGGAAAAGA TATCACTTTA AAAGCACTTA TTGAGGCTTC AATGACATAT	360
AGTGATAATA CAGCAAACAA TAAAATTATA AAAGAAATCG GTGGAATCAA AAAAGTTAAA	420
CAACGTCTAA AAGAACTAGG AGATAAGTA ACAAATCCAG TTAGATATGA GATAGAATTA	480
AATTACTATT CACCAAAGAG CAAAAAGAT ACTTCAACAC CTGCTGCTTT CGGTAAGACT	540
TTAAATAAAC TTATCGCAA TGGAAAATTA AGCAAAGAAA ACAAAAAATT CTTACTTGAT	600
TTAATGTAA ATAATAAAAG CGGAGATACT TTAATTAAAG ACGGTGTTCC AAAAGACTAT	660
AAGGTTGCTG ATAAAAGTGG TCAAGCAATA ACATATGCTT CTAGAAATGA TGTGCTTTT	720
GTTTATCCTA AGGGCCAATC TGAACCTATT GTTTTAGTCA TTTTACGAA TAAAGACAAT	780
AAAAGTGATA AGCCAAATGA TAAGTTGATA AGTGAAACCG CCAAGAGTGT AATGAAGGAA	840
TTTTAA	846

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

ATGTCCGCGA GCACCCCCC CATAACTCTT CGCCTCATGA CCGAGCGCGA CCTGCCGATG	60
CTCCATGACT GGCTCAACCG GCCGCACATC GTTGAGTGGT GGGGTGGCGA CGAAGAGCGA	120
CCGACTCTTG ATGAAGTGCT GGAACACTAC CTGCCCAGAG CGATGGCGGA AGAGTCCGTA	180
ACACCGTACA TCGCAATGCT GGGCGAGGAA CCGATCGGCT ATGCTCAGTC GTACGTCGCG	240
CTCGGAAGCG GTGATGGCTG GTGGGAAGAT GAAACTGATC CAGGAGTGCG AGGAATAGAC	300
CAGTCTCTGG CTGACCCGAC ACAGTTGAAC AAAGGCCTAG GAACAAGGCT TGTCCGCGCT	360

- 109 -

CTCGTTGAAC TACTGTTCTC GGACCCCACC GTGACGAAGA TTCAGACCGA CCCGACTCCG	420
AACAACCATC GAGCCATACG CTGCTATGAG AAGGCAGGAT TCGTGCGGGA GAAGATCATC	480
ACCACGCCTG ACGGGCCGGC GGTTTACATG GTTCAAACAC GACAAGCCTT CGAGAGAAAG	540
CGCGGTGTTG CCTAA	555

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ATGAACCAGA AAAACCCCTAA AGACACGCAA AATTTTATTA CTTCTAAAA GCATGTAAAA	60
GAAATATTGA ATCACACGAA TATCAGTAAA CAAGACAACG TAATAGAAAT CGGATCAGGA	120
AAAGGACATT TTACCAAAGA GCTAGTCAAA ATGAGTCGAT CAGTTACTGC TATAGAAATT	180
GATGGAGGCT TATGTCAAGT GACTAAAGAA GCGGTAAACC CCTCTGAGAA TATAAAAGTG	240
ATTCAAACGG ATATTCTAAA ATTTTCCTTC CCAAACATA TAAACTATAA GATATATGGT	300
AATATTCCTT ATAACATCAG TACGGATATT GTCAAAAGAA TTACCTTTGA AAGTCAGGCT	360
AAATATAGCT ATCTTATCGT TGAGAAGGGA TTTGCGAAAA GATTGCAAAA TCTGCAACGA	420
GCTTTGGGTT TACTATTAAT GGTGGAGATG GATATAAAAA TGCTCAAAAA AGTACCACCA	480
CTATATTTTC ATCCTAAGCC AAGTGTAGAC TCTGTATTGA TTGTTCTTGA ACGACATCAA	540
CCATTGATTT CAAAGAAGGA CTACAAAAAG TATCGATCTT TTGTTTATAA GTGGGTAAAC	600
CGTGAATATC GTGTTCTTTT CACTAAAAAC CAATTCCGAC AGGCTTTGAA GCATGCAAAT	660
GTCATAATA TTAATAAACT ATCGAAGGAA CAATTTCTTT CTATTTTCAA TAGTTACAAA	720
TTGTTTCACT AA	732

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 110 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

ATGAACAAAA ATATAAAATA TTCTCAAAAC TTTTTAACGA GTGAAAAAGT ACTCAACCAA	60
ATAATAAAAC AATTGAATTT AAAAGAAACC GATACCGTTT ACGAAATTGG AACAGGTAAA	120
GGGCATTTAA CGACGAAACT GGCTAAAATA AGTAAACAGG TAACGTCTAT TGAATTAGAC	180
AGTCATCTAT TCAACTTATC GTCAGAAAAA TTAAAATCGA ATACTCGTGT CACTTTAATT	240
CACCAAGATA TTCTACAGTT TCAATTCCTT AACAAACAGA GGTATAAAAT TGTTGGGAAT	300
ATTCCTTACC ATTTAAGCAC ACAAATTATT AAAAAAGTGG TTTTGTAAAG CCATGCGTCT	360
GACATCTATC TGATTGTTGA AGAAGGATTC TACAAGCGTA CCTTGGATAT TCACCGAACA	420
CTAGGGTTGC TCTTGACAC TCAAGTCTCG ATTCAGCAAT TGCTTAAGCT GCCAGCGGAA	480
TGCTTTCATC CTAAACCAAG AGTAAACAGT GTCTTAATAA AACTTACCCG CCATACCACA	540
GATGTTCCAG ATAAATATTG GAAGCTATAT ACGTACTTTG TTTCAAAATG GGTCAATCGA	600
GAATATCGTC AACTGTTTAC TAAAAATCAG TTTTCATCAAG CAATGAAACA CGCCAAAGTA	660
AACAATTTAA GTACCGTTAC TTATGAGCAA GTATTGTCTA TTTTAAATAG TTATCTATTA	720
TTTAACGGGA GGAAATAA	738

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

ATGAACGAGA AAAATATAAA ACACAGTCAA AACTTTATTA CTTCAAAACA TAATATAGAT	60
AAAATAATGA CAAATATAAG ATTAAATGAA CATGATAATA TCTTTGAAAT CGGCTCAGGA	120
AAAGGGCATT TTACCCTTGA ATTAGTACAG AGGTGTAATT TCGTAACTGC CATTGAAATA	180
GACCATAAAT TATGCAAAAC TACAGAAAAT AAAGTTGTTG ATCACGATAA TTTCCAAGTT	240
TTAAACAAGG ATATATTGCA GTTTAAATTT CCTAAAAACC AATCCTATAA AATATTTGGT	300
AATATACCTT ATAACATAAG TACGGATATA ATACGCAAAA TTGTTTTTGA TAGTATAGCT	360
GATGAGATTT ATTTAATCGT GGAATACGGG TTTGCTAAAA GATTATTAAA TACAAAACGC	420
TCATTGGCAT TATTTTAAAT GGCAGAAGTT GATATTTCTA TATTAAGTAT GGTCCAAGA	480

- 111 -

GAATATTTTC ATCCTAAACC TAGAGTGAAT AGCTCACTTA TCAGATTAAA TAGAAAAAAA	540
TCAAGAATAT CACACAAAGA TAAACAGAAG TATAATTATT TCGTTATGAA ATGGGTTAAC	600
AAAGAATACA AGAAAAATATT TACAAAAAAT CAATTTAACA ATTCCTTAAA ACATGCAGGA	660
ATTGACGATT TAAACAATAT TAGCTTTGAA CAATTCTTAT CTCTTTTCAA TAGCTATAAA	720
TTATTTAATA AGTAA	735

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

ATGAATAAAA TAAAAGTCGC AATTATCTTC GCGGTTGCT CGGAGGAACA TGATGTGTCG	60
GTAAATCCG CAATAGAAAT TGCTGCGAAC ATTAATACTG AAAAATTCGA TCCGCACTAC	120
ATCGGAATTA CAAAAACGG CGTATGGAAG CTATGCAAGA AGCCATGTAC GGAATGGGAA	180
GCCGATAGTC TCCCCGCCAT ATTCTCCCG GATAGGAAAA CGCATGGTCT GCTTGTCATG	240
AAAGAAAGAG AATACGAAAC TCGGCGTATT GACGTGGCTT TCCCGGTTTT GCATGGCAAA	300
TGCGGGGAGG ATGGTGCGAT ACAGGGTCTG TTTGAATTGT CTGGTATCCC CTATGTAGGC	360
TGCGATATTC AAAGCTCCGC AGCTTGCATG GACAAATCAC TGGCCTACAT TCTTACAAAA	420
AATGCGGGCA TCGCCGTCCC CGAATTTCOA ATGATTGAAA AAGGTGACAA ACCGGAGGCG	480
AGGACGCTTA CCTACCCTGT CTTTGTGAAG CCGGCACGGT CAGGTTGTC CTTTGGCGTA	540
ACCAAAGTAA ACAGTACGGA AGAACTAAAC GCTGCGATAG AAGCAGCAGG ACAATATGAT	600
GGAAAAATCT TAATTGAGCA AGCGATTTTCG GGCTGTGAGG TCGGCTGCGC GGTCATGGGA	660
AACGAGGATG ATTTGATTGT CGGCGAAGTG GATCAAATCC GGTGAGCCA CGGTATCTTC	720
CGCATCCATC AGGAAAACGA GCCGGAAAAA GGCTCAGAGA ATGCGATGAT TATCGTTCCA	780
GCAGACATTC CGGTGAGGGA ACGAAATCGG GTGCAAGAAA CGGCAAAGAA AGTATATCGG	840
GTGCTTGAT GCAGAGGGCT TGCTCGTGTT GATCTTTTTT TGCAGGAGGA TGGCGGCATC	900
GTTCTAAACG AGGTCAATAC CCTGCCCGGT TTACATCGT ACAGCCGCTA TCCACGCATG	960
GCGGCTGCCG CAGGAATCAC GCTTCCCGCA CTAATTGACA GCCTGATTAC ATTGGCGATA	1020

- 112 -

GAGAGGTGA

1029

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATGAAAAAAAA TTGCCGTTTT ATTTGGAGGG AATTCTCCAG AATACTCAGT GTCACTAACC	60
TCAGCAGCAA GTGTGATCCA AGCTATTGAC CCGCTGAAAT ATGAAGTAAT GACCATTGGC	120
ATCGCACCAA CAATGGATTG GTATTGGTAT CAAGGAAACC TCGCGAATGT TCGCAATGAT	180
ACTTGGCTAG AAGATCACAA AAAGTGTAC CAGCTGACTT TTTCTAGCCA AGGATTTATA	240
TTAGGAGAAA AACGAATCGT CCCTGATGTC CTCTTTCCAG TCTTGCATGG GAAGTATGGC	300
GAGGATGGCT GTATCCAAGG ACTGCTTGAA CTAATGAACC TGCCTTATGT TGGTTGCCAT	360
GTCGCTGCCT CCGCATTATG TATGAACAAA TGGCTCTTGC ATCAACTTGC TGATACCATG	420
GGAATCGCTA GTGCTCCAC TTTGCTTTTA TCCCGCTATG AAAACGATCC TGCCACAATC	480
GATCGTTTTA TTCAAGACCA TGGATTCCCG ATCTTTATCA AGCCGAATGA AGCCGGTTCT	540
TCAAAAGGGA TCACAAAAGT AACTGACAAA ACAGCGCTCC AATCTGCATT AACGACTGCT	600
TTTGCTTACG GTTCTACTGT GTTGATCCAA AAGGCGATAG CGGGTATTGA AATTGGCTGC	660
GGCATCTTAG GAAATGAGCA ATTGACGATT GGTGCTTGTG ATGCGATTTC TCTTGTCGAC	720
GGTTTTTTTTG ATTTTGAAGA GAAATACCAA TTAATCAGCG CCACGATCAC TGTCCCAGCA	780
CCATTGCCTC TCGCGCTTGA ATCACAGATC AAGGAGCAGG CACAGCTGCT TTATCGAAAC	840
TTGGGATTGA CGGGTCTGGC TCGAATCGAT TTTTTCGTCA CCAATCAAGG AGCGATTTAT	900
TTAAACGAAA TCAACACCAT GCCGGGATTT ACTGGGCACT CCCGCTACCC AGCTATGATG	960
GCGGAAGTCG GGTTATCCTA CGAAATATTA GTAGAGCAAT TGATTGCACT GGCAGAGGAG	1020
GACAAACGAT G	1031

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- 113 -

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Abiotrophia adiacens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

TGGTGCTATC TTAGTAGTAT CTGCAGCTGA TGGTCCAATG CCTCAAACAC GTGAACACAT	60
CTTATTATCA CGTCAAGTAG GTGTTCCTTA CATCGTTGTA TTCTTAAACA AAGTTGACAT	120
GGTTGACGAT GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTATCAGA	180
ATACGATTTT CCAGGCGATG AACTCCAGT TGTTCAGGT TCTGCTTTAC GCGCTTTAGA	240
AGGCGACGCT TCATACRAAG AAAAAATCTT AGAATTAATG GCTGCTGTTG ACGAATACAT	300
TCCAACCTCA GAACGYGACG TTGACAAACC ATTCATGATG CCAGTTGAAG ACGTGTCTC	360
AATCACAGGT CGTGGTACTG TTGCTACAGG TCGTGTGAA CGTGGACAAG TTCGTGTTGG	420
TGACGAAGTT GAAATCGTTG GTATTTTCTA AGAACTTCA AAAACAACCTG TAACTGGTGT	480
TGAAATGTTT CGTAAATTGT TAGACTACGC TGAAGCAGGG GATAACATTG GTACATTATT	540
ACGTGGTGTT ACACGTGACA ACATCGAACG TGGACAAGTT CTTGCTAAAC CAGGAACAAT	600
CACTCCACAT ACTAAATTCA AAGCTGAAGT TTACGTATTA ACTAAAGAAG AAGGTGGACG	660
TCATACTCCA TTCTTCTCTA ACTACCGTCC TCAATTCTAC TTCCGTACAA CAGACATCAC	720
TGGTGTTTGT GTGTTACCAG AAGGCGTTGA AATGGTAATG CCTGGTGATA ACGTAACTAT	780
GGAAGTTGAA TTAATTCACC CAGTAGCGA	809

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 817 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Abiotrophia defectiva*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

CGGCGCGATC CTCGTTGTAT CTGCTGCTGA CGGCCCAATG CCACAAACTC GTGAACACAT	60
CCTCTTGTCT CGTCAAGTTG GTGTTCCTTA CATCGTAGTA TTCTTGAACA AAGTTGACAT	120

- 114 -

GGTTGACGAC GAAGAATTGC TCGAATTAGT TGAAATGGAA GTTCGTGACC TCTTGTCTGA	180
ATACGACTTC CCAGGCGACG ACACTCCAGT TATCGCTGGT TCAGCTTTGA AAGCTTTAGA	240
AGGCGACGCT AACTACGAAG CTAAAGTTTT AGAATTGATG GAACAAGTTG ATGCTTACAT	300
TCCAGAACCA GAACGTGACA CTGACAAGCC ATTCATGATG CCAGTCGAAG ACGTATTCTC	360
TATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTGAA CGTGGTCAAG TTCGCGTTGG	420
TGACGAAGTT GAAATCGTTG GTATCGAAGA AGAACTTCT AAGACTACCG TTACCGGTGT	480
TGAAATGTTT CGTAAGTTAT TGGATTACGC TGAAGCTGGG GACAACGTTG GTACCTTGTT	540
ACGTGGTGTA ACTCGTGACC AAATCCAACG TGGTCAAGTA TTATCTAAAC CAGGTTCAAT	600
CACTCCGYAC ACTAAGTTCT AAGCTGAAGT GTACGTATTG TCTAAAGAAG AAGGTGGTCG	660
TCACACTCCA TTCTTCTCTA ACTACCGTCC ACAATTCTAC TTCCGTACAA CTGACGTAAC	720
TGGTGTGTT ACTTTACCAG AAGGTACTGA AATGGTTATG CCAGGCGACA ACGTACAAAT	780
GGTGTGTTGAA TTGATCCACC CAATCGCGAT CGAAGAA	817

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

CTCTGTCAAA TGGGACAAA ACAGATTTGA AGAAATCATC AAGGAAACCT CCAACTTCGT	60
CAAGAAGGTT GGTTACAACC CAAAGACTGT TCCATTCGTT CCAATCTCTG GTTGGAATGG	120
TGACAACWTG ATTGAASCAT CCACCAACTG TCCATGGTAC AAGGGTTGGG AAAAGGAAAC	180
CAAATCCGGT AAAGTTACTG GTAAGACCTT GTTAGAAGCT ATTGACGCTA TTGAACCACC	240
AACCAGACCA ACCGACAAAC CATTGAGATT GCCATTRCAA GATGTTTACA AGATCGGTGG	300
TATTGGTACT GTGCCAGTCG GTAGAGTTGA AACTGGTATC ATCAAAGCCG GTATGGTWGT	360
TACTTTCGCC CCAGCTGGTG TTACCACTGA AGTCAARTCC GTTGAAATGC ATCACGAACA	420
ATTGGCTGAA GGTGTTCCAG GTGACAATGT TRGTTTCAAC GTTAAGAACR TTTCCGTTAA	480
AGAAATTAGA AGAGGTAACG TTTGTGGTGA CTCCAAGAAC GATCCACCAA AGGGTTGTGA	540

- 115 -

CTCTTTCAAT GCCCAAGTCA TTGTTTTGAA CCATCCAGGT CAAATCTCTG CTGGTTACTC	600
TCCAGTCTTG GATTGTCACR CTGCCCACAT TGCTTGTAAG TTCGACRCTT TGTTGAAAA	660
GATTGACAGA AGAACTGGTA AGRAATTGGA AGAAAATCCA AAATTCGTCA AATCCGGTGA	720
TGCTGCTATC GTCAAGATGG TCCCAACCAA ACCA	754

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida glabrata*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

TCTGTCAAGT GGGATGAATC CAGATTCGCT GAAATCGTTA AGGAAACCTC CAACTTCATC	60
AAGAAGGTCG GTTACAACCC AAAGACTGTT CCATTCGTCC CAATCTCTGG TTGGAACGGT	120
GACAACATGA TTGAAGCCAC CACCAACGCT TCCTGGTACA AGGGTTGGGA AAAGGAAACC	180
AAGGCTGGTG TCGTCAAGGG TAAGACCTTG TTGGAAGCCA TTGACGCTAT CGAACCACCA	240
ACCAGACCAA CTGACAAGCC ATTGAGATTG CCATTGCAAG ATGTCTACAA GATCGGTGGT	300
ATCGGTACGG TGCCAGTCGG TAGAGTCGAA ACCGGTGTCA TCAAGCCAGG TATGGTTGTT	360
ACCTTCGCCC CAGCTGGTGT TACCACTGAA GTCAAGTCCG TTGAAATGCA CCACGAACAA	420
TTGACTGAAG GTTTGCCAGG TGACAACGTT GGTTTCAACG TTAAGAACGT TTCCGTTAAG	480
GAAATCAGAA GAGGTAATGT CTGTGGTGAC TCCAAGAACG ACCCACCAAA GGCTGCTGCT	540
TCTTTCAACG CTACCGTCAT TGTCTTGAAC CACCCAGGTC AAATCTCTGC TGGTTACTCT	600
CCAGTTTTTG ACTGTCACAC CGCCACATT GCTTGTAAGT TCGAAGAATT GTTGGAAGG	660
AACGACAGAA GATCCGGTAA GAAGTTGGAA GACTCTCCAA AGTTCTTGAA GTCCGGTGAC	720
GCTGCTTTTG TTAAGTTCGT TCCATCCAAG CCA	753

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- 116 -

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida krusei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```

CCGTTAAGTG GGATGAAAAC AGATTTGAAG AAATTGTCAA GGAAACCCAA AACTTCATCA      60
AGAAGGTTGG TTACAACCCA AAGACTGTTC CATTCGTTCC AATCTCTGGT TGGAATGGTG      120
ACAACATGAT TGAAGCATCC ACCAACTGTC CATGGTACAA GGGTTGGACT AAGGAAACCA      180
AGGCAGGTGT TGTTAAGGGT AAGACCTTAT TAGAAGCAAT CGATGCTATT GAACCACCTG      240
TCAGACCAAC CGAAAAGCCA TTAAGATTAC CATTACAAGA TGTTTACAAG ATTGGTGGTA      300
TTGGTACTGT GCCAGTCGGT AGAGTCGAAA CCGGTGTCAT TAAGCCAGGT ATGGTTGTCA      360
CTTTTGCTCC AGCAGGTGTC ACCACCGAAG TCAAATCCGT TGAAATGCAC CATGAACAAT      420
TAGAACAAGG TGTTCCAGGT GATAACGTTG GTTTCAACGT TAAGAACGTY TCTGTCAAGG      480
ATATCAAGAG AGGTAACGTT TGTGGTGACT CCAAGAACGA CCCACCAATG GGTGCAGCTT      540
CTTTCAATGC TCAAGTCATT GTCTTGAACC ACCCTGGTCA AATTTCGCT GGTACTCTC      600
CAGTCTTGGA TTGTCACACT GCCCACATTG CATGTAAGTT CGACGAATTA ATCGAAAAGA      660
TTGACAGAAG AACTGGTAAG TCTGTTGAAG ACCATCCAAA GTCYGTCAAG TCTGGTGATG      720
CAGCTATCGT CAAGATGGTC CCAACCAAGC CA                                     752

```

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida parapsilosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

CTCAGTCAAA TGGGACAAGA RCAGATACGA AGAAATTGTC AAGGAAACTT CCAACTTCGT      60
CAAGAAGGTT GGTTACAACC CTAAAGCTGT CCCATTCGTC CCAATCTCTG GTTGGAACGG      120
TGACAATATG ATTGAACCAT CAACCAACTG TCCATGGTAC AAGGGTTGGG AAAAGGAAAC      180
TAAAGCTGGT AAGGTTACCG GTAAGACCTT GTTGGAAGCT ATCGATGCTA TCGARCCACC      240

```

- 117 -

```

AACCAGACCA ACTGACAAGC CATTGAGATT GCCATTGCAA GATGTC'TACA AGATTGGTGG      300
TATTGGAAC'T GTGCCAGTTG GTAGAGTTGA AACC'GGTATC ATCAAGGCTG GTATGGTTGT      360
TACTTTT'GCC CCAGCTGGTG TTACCACTGA AGTCAAGTCC GTTGAAATGC ACCACGAACA      420
ATTGACTGAA GGTGTCC'AG GTGACAATGT TGGTTTCAAC GTCAAGAACG TTTCAGTTAA      480
GGAAATCAGA AGAGGTAACG TYTGTGGTGA CTCCAAGAAC GATCCACCAA AGGGATGTGA      540
YTCTTCAAT GCTCAAGTTA TTGTCTTGAA CCACCCAGGT CAAATCTCTG CTGGTTACTC      600
ACCAGTCTTG GATTGTCACA CTGCCCACAT TGCTTGTA'AA TTCGACACTT TGATTGAAAA      660
GATTGACAGA AGAACCGGTA AGAAATTGGA AGWTGAACCA AAATTCATCA AGTCCGGTGA      720
TGCTG'CYATC GTCAAGATGG TCCCAACCAA GCCA                                     754

```

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```

TCTGT'TAAAT GGGACAARAA CAGATTTGAA GAAAT'TATCA AGGAAACYTC TAACTTCGTC      60
AAGAAGGTTG GTTACAACCC TAAGGCTGTT CCATTCGTTT CAATCTCWGG TTGGAATGGT      120
GACAACATGA TTGAAGCTTC TACCAACTGT CCATGGTACA AGGGT'TGGGA AAAAGAAACC      180
AAGGCTGGTA AGGT'TACCGG TAAGACTTTG TTGGAAGCCA TTGATGCTAT TGAACCACCT      240
TCAAGACCAA CTGACAAGCC ATTGAGATTG CCATTGCAAG ATGTTTACAA GATTGGTGGT      300
ATTGGTACTG TGCCAGTCGG TAGAGTTGAA ACTGGTGTCA TCAAAGCCGG TATGGTTGTT      360
ACTTTYGCCC CAGCTGGTGT TACCACTGAA GTCAAATCCG TYGAAATGCA CCACGAACAA      420
TTGGCTGAAG GTGTCCCAGG TGACAATGTT GGT'TTCAACG TTAAGAACGT TTCTGT'TAA      480
GAAAT'TAGAA GAGGTAACGT TTGTGGTGAC TCCAAGAACG ATCCACCAA GGGTTGTGAC      540
TCTTTCAACG CTCAAGTTAT TGTCTTGAAC CACCCAGGTC AAATYTCTGC TGTTACTCT      600
CCAGTCTTGG ATTGTCACAC TGCTCATATT GCTTGTA'AT TCGACACCTT GGTTGAAAAG      660
ATTGACAGAA GAACTGGTAA GAAATTGGAA GAAAATCCAA AATTCGTCAA ATCCGGTGAT      720

```

- 118 -

GCTGCTATTG TCAAGATGGT TCCAACCAAA CCA

753

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium accolens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

CGGCGCTATC CTGGTTGTTG CTGCAACCGA TGGCCCGATG CCGCAGACCC GCGAGCACGT	60
TCTGCTTGCT CGCCAGGTTG GCGTTCCTTA CATCCTCGTT GCACTGAACA AGTGCGACAT	120
GGTTGATGAT GAGGAAATCA TCGAGCTCGT GGAGATGGAG ATCTCCGAGC TGCTCGCAGA	180
GCAGGACTAC GATGAGGAAG CTCCTATCGT TCACATCTCC GCTCTGAAGG CACTCGAGGG	240
TGACGAGAAG TGGGTACAGT CCATCGTTGA CCTGATGGAT GCCTGCGACA ACTCCATCCC	300
TGATCCGGAG CGCGCTACCG ATCAGCCGTT CTTGATGCCT ATCGAGGACA TCTTCACCAT	360
TACCGGCCGC GGTACCGTTG TTACCGGCCG TGTGAGCGT GGTCGTCTGA ACGTCAACGA	420
GGACGTTGAG ATCATCGGTA TCCAGGAGAA GTCCCAGAAC ACCACCGTTA CCGGTATCGA	480
GATGTTCCGC AAGATGATGG ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTGCG	540
TGGTACCAAG CGTGAGGACG TTGAGCGTGG CCAGGTTGTT ATCAAGCCGG GCGCTTACAC	600
CCCTCACACC AAGTTCGAGG GTTCCGTCTA CGTCTGAAG AAGGAAGAGG GCGGCCGCCA	660
CACCCCGYTC ATGAACAACT ACCGTCCTCA GTTCTACTTC CGCACCACCG ACGTTACCGG	720
TGTTGTGAAC CTGCCTGAGG GCACCGAGAT GGTATGCCT GCGACAACG TTGAGATGTC	780
TGTTGAGCTC ATCCAGCCTG TTGCTATGGA CGAG	814

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 119 -

(A) ORGANISM: *Corynebacterium diphtheriae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

CGGCGCAATC CTCGTTGTTG CTGCCACCGA CGGCCCAATG CCTCAGACCC GTGAGCACGT	60
TCTGCTCGCT CGCCAGGTCG GCGTTCCTTA CATCCTCGTT GCTCTGAACA AGTGCGACAT	120
GGTTGATGAT GAGGAAATCA TCGAGCTCGT CGAGATGGAG ATCCRTGAGC TGCTCGCTGA	180
GCAGGATTAC GACGAAGAGG CTCCAATCAT CCACATCTCC GCACTGAAGG CTCTTGAGGG	240
CGACGAGAAG TGGACCCAGT CCATCATCGA CCTCATGCAG GCTTGCKATG ATTCCATCCC	300
AGACCCAGAG CGTGAGACCG ACAAGCCATT CCTCATGCCT ATCGAGGACA TCTTCACCAT	360
CACCGGCCGC GGTACCGTTG TTACCGGCCG TGTGAGCGT GGCTCCCTGA AGGTCAACGA	420
GGACGTCGAG ATCATCGGTA TCCGCGAGAA KGCTACCACC ACCACCGTTA CCGGTATCGA	480
GATGTTCCGT AAGCTTCTCG ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTCCG	540
TGGCGTTAAG CGCGAAGACG TTGAGCGTGG CCAGGTTGTT GTTAAGCCAG GCGCTTACAC	600
CCCTCACACC GAGTTCGAGG GCTCTGTCTA CGTTCTGTCC AAGGACGAGG GTGGCCGCCA	660
CACCCCATTC TTCGACAACT ACCGCCCACA GTTCTACTTC CGCACCACCG ACGTTACCGG	720
TGTTGTGAAG CTTCTGAGG GCACCGAGAT GGTCATGCCT GGCACAAACG TCGACATGTC	780
CGTCACCCTG ATCCAGCCTG TCGCTATGGA TGAG	814

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium genitalium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

CGGCGCCATC CTGGTTGTTG CTGCAACCGA TGGCCCGATG CCGCAGACCC GTGAGCACGT	60
TCTGCTGGCT CGCCAGGTTG GCGTTCGGTA CATCCTAGTT GCACTGAACA AGTGCGACAT	120
GGTTGATGAT GAGGAGCTGC TGGAGCTCGT CGAGATGGAG GTCCGCGAGC TGCTGGCTGA	180
GCAGGACTTC GACGAGGAAG CACCTGTTGT TCACATCTCC GCACTGAAGG CCCTGGAGGG	240
CGACGAGAAG TGGGCTAAGC AGATCCTGGA GCTCATGGAG GCTTGCGACA ACTCCATCCC	300

- 120 -

GGATCCGGAG CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGRGGACA TCTTCACCAT 360
 TACCGGCCGC GGTACCGTTG TTACCGGCCG TGTGAGCGT GGCCTCCTGA ACCTGAACGA 420
 CGAGGTCGAG ATCCTGGGCA TCCGCGAGAA GTCCACCAAG ACCACCGTTA CCTCCATCGA 480
 GATGTTCAAC AAGCTGCTGG ACACCGCAGA GGCTGGCGAC AACGCCGCAC TGCTGCTGCG 540
 TGGCCTGAAG CGCGAAGATG TTGAGCGTGG TCAGATCGTT GCTAAGCCGG GCGAGTACAC 600
 CCCGCACACC GAGTTCGAGG GCTCCGTCTA CGTTCTGTCC AAGGACGAGG GTGGCCGCCA 660
 CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTATTTC CGCACCACCG ACGTTACCGG 720
 TGTGTGAAG CTGCCGGAGG GCACCGAGAT GGTATGCCG GCGACAACG TTGACATGTC 780
 CGTCACCCTG ATCCAGCCGG TTGCTATGGA CGAG 814

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium jeikeium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CGGCGCCATC CTGGTTGTTG CCGCAACCGA TGGCCCAGATG CCGCAGACCC GCGAGCACGT 60
 TCTGCTGGCY CGCCAGGTTG GCGTTCCGTA CATCCTGGTT GCACTGAACA AGTGTGACAT 120
 GGTGACGAT GAGGAGCTGC TGGAGCTCGT CGAGATGGAG GTCCGCGAGC TGCTGGCTGA 180
 GCAGGACTTC GACGAGGAAG CTCCGTTGT TCACATCTCC GCACTGAAGG CCCTGGAGGG 240
 CGACGAGAAG TGGGCTAACC AGATTCTCGA GCTGATGCAG GCTTGCGACG AGTCTATCCC 300
 GGATCCGGAG CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGWGGACA TCTTCACCAT 360
 TACCGGTCGC GGTACCGTTG TTACCGGCCG TGTGAGCGT GGCATCCTGA ACCTGAACGA 420
 CGAGGTTGAG ATCCTGGGTA TCCGCGAGAA GTCCAGAAG ACCACCGTTA CCTCCATCGA 480
 GATGTTCAAC AAGCTGCTGG ACACCGCAGA GGCTGGCRAC AACGCTGCAC TGCTGCTGCG 540
 TGGTCTGAAG CGCGAGGACG TTGAGCGTGG CCAGATCATC GCTAAGCCGG GCGAGTACAC 600
 CCCGCACACC GAGTTCGAGG GCTCCGTCTA CGTTCTGTCC AAGGACGAGG GCGGCCGCCA 660
 CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTACTTC CGCACCACCG ACGTTACCGG 720

- 121 -

TGTTGTGAAG CTGCCTGAGG GCACCGAGAT GGTATGCCG GCGACAACG TYGACATGTC 780
 CGTCACCCCTG ATCCAGCCGG TTGCTATGGA CGAG 814

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

CGGCGCTATC TTGGTTGTTG CAGCTACCGA CGGCCCAATG CCACAGACTC GCGAGCACGT 60
 TCTGCTGGCT CGCCAGGTTG GCGTTCCTTA CATCCTGGTT GCACTAAACA AGTGCGACAT 120
 GGTTGACGAC GAGGAAATCC TCGAGCTCGT CGAGATGGAG ATCCGCGAAT TGCTGGCTGA 180
 CCAGGAATTC GACGAAGAAG CTCCAATCGT TCACATCTCC GCAGTCGGCG CCTTGGAAGG 240
 CGAAGAGAGG TGGGTTAACG CCATCGTTGA ACTGATGGAT GCTTGTGACG AGTCGATCCC 300
 TGATCCAGAC CGTGCTACCG ACAAGCCATT CCTGATGCCT ATCGAGGACA TCTTCACCAT 360
 TACCGGTCGT GGCACCGTTG TTACGGGTCG TGTTGAGCGT GGTTCCTGA AGGTCAACGA 420
 AGAAGTCGAG ATCATCGGCA TCAAGGAAAA GTCCAGAAG ACCACCATCA CCGGTATCGA 480
 AATGTTCCGC AAGATGCTGG ACTACACCGA GGCCGGCGAC AACGCTGGTC TGCTGCTTCG 540
 CGGTACCAAG CGTGAAGACG TTGAGCGTGG ACAGGTTATC GTTGCTCCAG GTGCTTACAG 600
 CACCCACAAG AAGTTCGAAG GTTCCGTCTA CGTTCTTTCC AAGGACGAGG GCGGCCGCCA 660
 CACCCCGTTC TTCGACAACT ACCGTCCTCA GTTCTACTTC CGCACCACCG ACGTTACCGG 720
 TGTTGTTACC CTGCCTGAGG GCACCGAG 748

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 122 -

(A) ORGANISM: *Corynebacterium striatum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

```

GGCGCTATCT TGGTTGTTGC TGCAACCGAT GGCCCGRTGC CGCAGACCCG CGAGCACGTT      60
CTTCTGGCTC GCCAGGTTGG CGTTCCTTAC ATCCTCGTTG CACTGAACAA GTGCGACATG      120
GTTGACGACG AGGAAATTAT CGAGCTCGTC GAGATGGAGA TCCGCGAACT GCTCGCAGAG      180
CAGGACTACG ATGAGGAAGC TCCGATCGTT CACATCTCTG CTCTGAAGGC TCTTGAGGGC      240
GRCGAGAAGT GGGTACAGGC TATCGTTGAC CTGATGCAGG CTTGCGATGA CTCCATCCCG      300
GATCCGGAGC GCGAGCTGGA CAAGCCGTTT CTGATGCCAA TCGAGGACAT CTTCACCATC      360
ACCGGCCGCG GTACCGTTGT TACTGGCCGT GTTGAGCGTG GCTCCCTGAA CGTCAACGAG      420
GACGTTGAGA TCATCGGTAT CCAGGACARG TCCATCTCCA CCACCGTTAC CGGTATCGAG      480
ATGYTCCGCA AGATGATGGA CTACACCGAG GCTGGCGACA ACTGTGGTCT GCTTCTGCGT      540
GGTACCAAGC GTGAAGAGGT TGAGCGCGGC CAGGTTGTTA TTAAGCCGGG CGCTTACACC      600
CCTCACACCC AGTTCGAGGG TTCCGTCTAC GTCCTGAAGA AGGAAGAGGG CGGCCGCCAC      660
ACCCCGTTCA TGGACAAC TA CCGTCCGCAG TTCTACTTCC GCACCACCGA CGTTACCGGC      720
GTCATCAAGC TGCCTGAGGG CACCGAGATG GTTATGCCTG GCGACAACGT CGAGATGTCY      780
GTCGAGCTGA TCCAGCCGGT CGCTATGGAC GAG                                     813

```

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCTATG CCTCAAAC TC GTGAACACAT      60
CTTGTTATCT CGTAACGTTG GTGTTCTTCA CATCGTTGTA TTCTTAAACA AAATGGATAT      120
GGTTGACGAT GAAGAATTAC TTGAATTAGT TGAAATGGAA GTTCGTGACT TATTAAGTGA      180
ATACGACTTC CCAGGCGACG ACACTCCAGT TATCGCAGGT TCAGCGTTGA AAGCTTTAGA      240
AGGCGACGCT TCATACGAAG AAAAAATCTT AGAATTAATG GCTGCTGTTG ACGAATATAT      300

```

- 123 -

```

CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG ACGTATTCTC      360
AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTTGAA CGTGGACAAG TTCGCGTTGG      420
TGACGAAGTT GAAATCGTAG GTATCGCTGA CGAAACTGCT AAAACAACCTG TTACAGGTGT      480
TGAAATGTTT CGTAAATTGT TAGACTACGC TGAAGCAGGT GACAACATCG GTGCTTTGTT      540
ACGTGGTGTT GCACGTGAAG ATATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT      600
CACTCCACAT AAAAAATTCT CTGCAGAAGT TTATGTTCTA ACTAAAGAAG AAGGTGGACG      660
TCATACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC TTCCGTACAA CTGACGTAAC      720
TGGTGTAGTT GATCTACCAG AAGGTACTGA AATGGTWATG CCTGGGGATA ACGTAACTAT      780
GGAAGTTGAA TTGATYCACC CAATYCGGGT AGAAGAC                                817

```

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```

CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGTCCTATG CCTCAAACAC GTGAACATAT      60
CTTATTATCA CGTAACGTTG GTGTACCATA CATCGTTGTA TTCTTAAACA AAATGGATAT      120
GGTTGATGAC GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTATCAGA      180
ATACGATTTT CCAGGCGATG ATGTTCCAGT TATCGCAGGT TCTGCTTTGA AAGCTTTAGA      240
AGGCGACGAG TCTTATGAAG AAAAAATCTT AGAATTAATG GCTGCAGTTG ACGAATATAT      300
CCCAACTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG ACGTATTCTC      360
AATCACTGGA CGTGGTACTG TTGCTACAGG ACGTGTTGAA CGTGGTGAAG TTCGCGTTGG      420
TGACGAAGTT GAAATCGTTG GTATTAAAGA CGAAACATCT AAAACAACYG TTACAGGTGT      480
TGAAATGTTT CGTAAATTAT TAGACTACGC TGAAGCAGGC GACAACMTCG GTGCTTTATT      540
ACGTGGTGTA GCACGTGAAG ATATCGAACG TGGACAAGTA TTAGCTAAAC CAGCTACAAT      600
CACTCCACAC AAAAAATTCA AAGCTGAAGT ATACGTATTA TCAAAAGAAG AAGGCGGACG      660
TCACACTCCA TTCTTCACTA ACTACCGTCC TCAATTCTAC TTCCGTACAA CAGACGTTAC      720

```

- 124 -

TGGTGTGTA GAATTGCCAG AAGGTACTGA AATGGTAATG CCTGGTGATA ACGTTGCTAT 780

GGACGTTGAA TTAATTCACC CAATCGCTAT CGAAGAC 817

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CGGAGCTATC TTGGTAGTTT CTGCTGCTGA CGGCCCAATG CCTCAAACCTC GTGAACACAT 60

CCTATTGTCT CGTCAAGTTG GTGTTCCCTTA CATCGTTGTA TTCTTGAACA AAGTAGACAT 120

GGTTGATGAC GAAGAATTAC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTAACAGA 180

ATACRAATTC CCTGGTGRCG ATGTTCCCTGT AGTTGCTGGA TCAGCTTTGA AAGCTCTAGA 240

AGGCGACGCT TCATACGAAG AAAAAATTCT TGAATTAATG GCTGCAGTTG ACGAATACAT 300

CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTTGAAG ACGTGTTCCTC 360

AATTACTGGA CGTGGTACTG TTGCTACAGG TCGTGTTGAA CGTGGACAAG TTCGCGTTGG 420

TGACGAAGTT GAAGTTGTTG GTATTGCTGA AGAACTTCA AAAACAACAG TTACTGGTGT 480

TGAAATGTTT CGTAAATTGT TAGACYACGC TGAAGCTGGA GACRACATTG GTGCTTTACT 540

ACGTGGTGTT GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT 600

CACACCTCRT AAAAAATTCT CTGCAGAAGT ATACGTGTTG ACAAAGAAG AAGGTGGACG 660

TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC TTCCGTACAA CTGACGTAAC 720

AGGTGTTGTT GAATTACCAG AAGGAACTGA AATGGTCATG CCCGGTGACA ACGT 774

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 125 -

(A) ORGANISM: *Enterococcus gallinarum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

CGGTGCGATC TTAGTAGTAT CTGCTGCTGA CGGTCCTATG CCTCAAACCTC GTGAACACAT	60
CTTGTTATCA CGTAACGTTG GCGTACCATA CATCGTTGTT TTCTTGAACA AAATGGATAT	120
GGTTGAYGAC GAAGAATTGC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTGTCTGA	180
ATATGACTTC CCAGGCGACG ATGTTCTGT AATCGCCGGT TCTGCTTTGA AAGCTCTTGA	240
AGGAGATCCT TCATACGAAG AAAAAATCAT GGAATTGATG GCTGCAGTTG ACGAATACGT	300
TCCAACTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG ACGTATTCTC	360
AATCACTGGA CGTGGTACTG TTGCTACAGG CCGTGTTGAA CGTGGACAAG TTCGCGTTGG	420
TGATGAAGTA GAAATCGTTG GTATTGCTGA CGAAACTGCT AAAACAACCTG TAACAGGTGT	480
TGAAATGTTT CGTAAATTGT TAGACTATGC TGAAGCAGGG GATAACATTG GTGCATTGCT	540
ACGTGGGGTT GCTCGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAG CTGGTACAAT	600
CACACCTCAT AAAAAATTCA AAGCTGAAGT TTATGTTTTG ACAAAGAAG AAGGTGGACG	660
TCACACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC TTCCGTACAA CTGACGTAAC	720
TGGTGTGTTT GAATTACCAG AAGGAACTGA AATGGTGATG CCTGGCGACA ACGTGACCAT	780
CGACGTTGAA TTGATRCACC CAATCGCTC	809

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gardnerella vaginalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

TGGCGCAATC CTCGTGGTTG CTGCTACCGA CGGTCCAATG GCTCAGACCC GTGAACACGT	60
CTTGCTTGCT AAGCAGGTCG GCGTTCCAAA AATTCTTGTT GCTTTGAACA AGTGCGATAT	120
GGTTGACGAC GAAGAGCTTA TCGATCTCGT TGAAGAAGAG GTCCGTGACC TCCTCGAAGA	180
AAACGGCTTC GATCGCGATT GCCCAGTCYT CCGTACTTCC GCTTACGGCG CTTTGATGA	240
TGACGCTCCA GACCACGACA AGTGGGTAGA GACCGTCAAG GAACTCATGA AGGCTGTTGA	300

- 126 -

CGAGTACATC CCAACCCCAA CTCACGATCT TGACAAGCCA TTCTTGATGC CAATCGAAGA 360
 TGTGTTCAACC ATCTCCGGTC GTGGTYCCGT TGTCAACCGGT CGTGTTGAGC GTGGTAAGCT 420
 CCCAATCAAC ACCCCAGTTG AGATCGTTGG TTTGCGCGAT ACCCAGACCA CCACCGTCAC 480
 CTCTATCGAG ACCTTCCACA AGCAGATGGA TGAGGCAGAG GCTGGCGATA ACACTGGTCT 540
 TCTTCTCCGC GGTATCAACC GTACCGACGT TGAGCGTGGT CAGGTTGTGG CTGCTCCAGG 600
 TTCTGTGACT CCACACACCA AGTTCGAAGG CGAAGTTTAC GTCTTGACCA AGGACGAAGG 660
 TGGCCGTCAC TCGCCATTCT TCTCCAACTA CCGTCCACAG TTCTACTTCC GTACCACCGA 720
 TGTTACTGGC GTTATCACCT TGCCAGACGG CATCGAAATG GTTCAGCCAG GCGATCACGC 780
 AACCTTCACT GTTGAGTTGA TCCAGGCTAT CGCAATGGAA GAG 823

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria innocua*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACATAT 60
 CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT 120
 GGTGACGAT GAAGAATTAC TAGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA 180
 ATATGAATTC CCTGGCGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA 240
 AGGTGAAGCT GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT 300
 TCCAACCTCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC 360
 AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGTTGAA CGTGGACAAG TTAAAGTTGG 420
 TGACGAAGTA GAAGTTATCG GTATTGAAGA AGAAAGCAAA AAAGTAGTAG TAACTGGAGT 480
 AGAAATGTTC CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT 540
 ACGTGGTGTT GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTAGCTAAAC CAGGTTTCGAT 600
 TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG AAGGTGGACG 660
 TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC 720

- 127 -

TGGTATTGTT ACACTTCCAG AAGGTACTGA AATGGTAATG CCTGGTGATA ACATTGAGCT 780
 TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC 817

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria ivanovii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAACTC GTGAACATAT 60
 TCTTACTTTC ACGTCAAGTT GGTGTTCCAT ACATCGTTGT ATTCATGAAC AAATGTGACA 120
 TGGTTGACGA TGAAGAATTA CTTGAATTAG TTGAAATGGA AATTCGTGAT CTATTAAGTG 180
 AATATGAATT CCCTGGCGAC GACATTCCTG TAATCAAAGG TTCAGCTCTT AAAGCACTTC 240
 AAGGTGAAGC TGATTGGGAA GCTAAAATTG ACGAGTTAAT GGAAGCTGTA GATTCTTACA 300
 TTCCAACCTC AGAACGTGAT ACTGACAAAC CATTCATGAT GCCAGTTGAG GATGTATTCT 360
 CAATCACTGG TCGTGGAACA GTTGCAACTG GACGTGTTGA ACGTGGACAA GTTAAAGTTG 420
 GTGACGAAGT AGAAGTTATC GGTATTGAAG AAGAAAGCAA AAAAGTAGTA GTAAGTGGAG 480
 TAGAAATGTT CCGTAAATTA CTAGACTACG CTGAAGCTGG CGACAACATT GGCGCACTTC 540
 TACGTGGTGT TGCTCGTGAA GATATCCAAC GTGGTCAAGT ATTAGCTAAA CCAGGTTCTGA 600
 TTACTCCACA TACTAACTTC AAAGCTGAAA CTTATGTTTT AACTAAAGAA GAAGGTGGAC 660
 GTCATACTCC ATTCTTCAAC AACTACCGCC CACAATTCTA TTTCCGTACT ACTGACGTAA 720
 CTGGTATTGT TAACTTCCA GAAGGTACTG AAATGGTAAT GCCTGGTGAT AACATTGAGC 780
 TTGCAGTTGA ACTAATTGCA CCAATCGCTA TCGAAGAC 818

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 128 -

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACATAT	60
CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT	120
GGTTGACGAT GAAGAATTAC TAGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA	180
ATATGAATTC CCTGGCGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA	240
AGGTGAAGCT GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT	300
TCCAACCTCCW GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC	360
AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGTTGAA CGTGGACAAG TTAAAGTTGG	420
TGACGAAGTA GAAGTTATCG GTATCGAAGA AGAAAGCAAA AAAGTAGTAG TAACTGGAGT	480
AGAAATGTTT CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT	540
ACGTGGTGTT GCTCGTGAAG ATATCCAACR TGGTCAAGTA TTAGCTAAAC CAGGTTTCGAT	600
TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG AAGGTGGACG	660
TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC	720
TGGTATTGTT ACACTTCCAG AAGGTACTGA AATGGTAAYG CCTGGTGATA ACATTGAGCT	780
TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC	817

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria seeligeri*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACATAT	60
CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT	120
GGTTGACGAT GAAGAATTAC TTGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA	180
ATATGAATTC CCTGGTGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA	240

- 129 -

AGGTGAAGCT GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT	300
TCCAACCTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC	360
AATCACTGGT CGTGGAACTG TTGCAACTGG ACGTGTTGAA CGTGGACAAG TTAAAGTTGG	420
TGACGAAGTA GAAGTTATCG GTATTGAAGA AGAAAGCAAA AAAGTAATAG TAACTGGAGT	480
AGAAATGTTT CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT	540
ACGTGGTGTT GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTAGCTAAAC CAGGTTTCGAT	600
TACTCCACAT ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG AAGGTGGACG	660
TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC	720
TGGTATTGTT ACACTTCCAG AAGGTACTGA AATGGTAATG CCTGGTGATA ACATTGAGCT	780
TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC	817

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

CGGTGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCACAAACTC GTGAACACAT	60
TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA TTCTTAAACA AAGTTGACAT	120
GGTTGACGAT GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTAAGCGA	180
ATATGACTTC CCAGGTGACG ATGTACCTGT AATCGCTGGT TCAGCATTAR AAGCTTTAGA	240
AGGCGATGCT CAATACGAAG AAAAAATCTT AGAATTARTG GAAGCTGTAG ATACTTACAT	300
TCCAACCTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC	360
AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA CGTGGTCAAA TCAAAGTTGG	420
TGAAGAAGTT GAAATCATCG GTTTACATGA CACATCTAAA ACAACTGTTA CAGGTGTTGA	480
AATGTTCCGT AAATTATTAG ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG	540
TGGTGTGCT CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC	600
ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG GTGGACGTCA	660

- 130 -

CACTCCATTC TTCTCAAAC ATCGTCCACA ATTCTATTTT CGTACTACTG ACGTAACTGG	720
TGTTGTTTAC TTACCAGAAG GTACTGAAAT GGTAATGCCT GGTGATAACG TTGAAATGAC	780
AGTAGAATTA ATCGCTCCAA TCGCGATTGA AGAC	814

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

CGGCGGTATC TTAGTTGTAT CTGCTGCTGA CGGTCCAATG CCACAACTC GTGAACACAT	60
CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA TTCTTAAACA AAGTTGACAT	120
GGTAGACGAC GAAGAATTAT TAGAATTAGT TGAAATGGAA GTTCGTGACT TATTAAGCGA	180
ATATGACTTC CCAGGTGACG ATGTACCTGT AATCGCTGGT TCTGCATTAA AAGCATTAGA	240
AGGCGATGCT GAATACGAAC AAAAAATCTT AGACTTAATG CAAGCAGTTG ATGATTACAT	300
TCCAACTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC	360
AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA CGTGGTCAAA TCAAAGTWGG	420
TGAAGAAGTT GAAATCATCG GTATGCACGA AACTTCTAAA ACAACTGTTA CTGGTGTAGA	480
AATGTTCCGT AAATTATTAG ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG	540
TGGTGTTGCA CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCTATTAC	600
ACCACACACA AAATTCAAAG CTGAAGTATA CGTATTATCT AAAGATGAAG GTGGACGTCA	660
CACTCCATTC TTCTAACT ATCGCCACA ATTCTATTTT CRTACTACTG ACGTAACTGG	720
TGTTGTAAAC TTACCAGAAG GTACAGAAAT GGTTATGCCT GGCGACAACG TTGAAATGAC	780
AGTTGAATTA ATCGCTCCAA TCGCTATCGA AGAC	814

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- 131 -

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACACAT	60
TCTTTTATCA CGTRACGTTG GTGYTCCAGC ATTAGTTGTA TTCTTAAACA AAGTTGACAT	120
GGTTGACGAY GAAGAATTAT TAGAATTRGT AGAAATGGAA GTTCGTGRCT TATTAAGCGA	180
ATATGACTTC CCAGGTGACG ATGTACCTGT AATCTCTGGT TCTGCATTAA AAGCTTTAGA	240
AGGCGACGCT GACTATGAGC AAAAAATCTT AGACTTAATG CAAGCTGTTG ATGACTYCAT	300
TCCAACACCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC	360
AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA CGTGGTCAAA TCAAAGTCGG	420
TGAAGAAATC GARATCATCG GTATGCAAGA AGAATCAAGC AAAACAACTG TTACTGGTGT	480
AGAAATGTTC CGTAAATTAT TAGACTACGC TGAAGCTGGT GACAACATTG GTGCATTATT	540
ACGTGGTGTT TCACGTGATG ATGTACAACG TGGTCAAGTT TTAGCTGCTC CTGGTACTAT	600
CACACCACAT ACAAATTCA AAGCGGATGT TTACGTTTTA TCTAAAGATG AAGGTGGTCG	660
TCATACGCCA TTCTTCACTA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC	720
TGGTGTTGTT AACTTACCAG AAGGTACTGA AATGGTTATG CCTGGCGATA ACGTTGAAAT	780
GGATGTTGAA TTAATTTCTC CAATCGCTAT TGAAGAC	817

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 817 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus simulans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

CGGCGGTATC TTAGTAGTAT CTGCTGCAGA TGGTCCAATG CCACAAACTC GTGAACACAT	60
CTTATTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA TTCTTAAACA AAGCTGACAT	120
GGTTGACGAC GAAGAATTAT TAGAATTAGT TGAAATGGAA GTTCGTGACT TATTATCTGA	180

- 132 -

ATACGACTTC	CCTGGTGACG	ATGTACCAGT	TATCGTTGGT	TCTGCATTAA	AAGCTTTAGA	240
AGGCGACCCA	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCTGTAG	ATGACTACAT	300
CCCAACTCCA	GAACGTGACT	CTGATAAACC	ATTCATGATG	CCAGTTGAGG	ACGTATTCTC	360
AATCACTGGT	CGTGGTACTG	TAGCAACAGG	CCGTGTTGAA	CGTGGTCAAA	TCAAAGTCGG	420
TGAAGAAGTT	GAAATCATCG	GTATCACTGA	AGAAAGCAAG	AAAACAACAG	TTACAGGTGT	480
AGAAATGTTT	CGTAAATTAT	TAGACTACGC	TGAAGCTGGT	GACAACATCG	GTGCTTTATT	540
ACGTGGTGTT	GCACGTGAAG	ACGTACAACG	TGGACAAGTA	TTAGCAGCTC	CTGGCTCTAT	600
TACTCCACAC	ACAAAATTCA	AAGCTGATGT	TTACGTTTTA	TCTAAAGAAG	AAGGTGGACG	660
TCATACTCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAC	TTCCGTACTA	CTGACGTAAC	720
TGGCGTTGTT	CACTTACCAG	AAGGTACTGA	AATGGTTATG	CCTGGCGATA	ACGTAGAAAT	780
GACTGTTGAA	TTGATCGCTC	CAATCGCGAT	TGAAGAC			817

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

CGGAGCTATC	CTTGTAAGTTG	CTTCAACTGA	TGGACCAATG	CCACAAACTC	GTGAGCACAT	60
CCTTCTTTCA	CGTCAAGTTG	GTGTTAAACA	CCTTATCGTA	TTCATGAACA	AAGTTGACCT	120
TGTTGATGAT	GAAGAATTGC	TTGAATTGGT	TGAAATGGAA	ATTCGTGACC	TTCTTTCAGA	180
ATACGACTTC	CCAGGTGATG	ACCTTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCACTTGA	240
AGGCGACGAA	AAATACGAAG	ACATCATCAT	GGAATTGATG	AGCACTGTTG	ATGAGTACAT	300
TCCAGAACCA	GAACGTGATA	CTGACAAACC	TTTACTTCTT	CCAGTTGAAG	ATGTATTCTC	360
AATCACTGGA	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAC	CGTGGTACTG	TTCGTGTCAA	420
CGACGAAGTT	GAAATCGTTG	GTATTAAAGA	AGATATCCAA	AAAGCAGTTG	TTACTGGTGT	480
TGAAATGTTT	CGTAAACAAC	TTGACGAAGG	TCTTGCAGGG	GACAACGTTG	GTGTTCTTCT	540
TCGTGGTGTT	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600

- 133 -

CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT TCTAAAGAAG AAGGTGGACG	660
TCATACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC TTCCGTACAA CTGACGTAAC	720
AGGTTCAATC GAACTTCCAG CAGGAACAGA AATGGTTATG CCTGGTGATA ACGTTACTAT	780
CGAAGTTGAA TTGATTCACC CAATCGCCGT AGAACAA	817

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

CGGAGCTATC CTTGTAGTAG CTTCAACTGA CGGACCAATG CCACAACTC GTGAGCACAT	60
CCTTCTTTCA CGTCAGGTTG GTGTAAACA CTTATCGTC TTCATGAACA AAGTTGACTT	120
GGTTGACGAC GAAGAATTGC TTGAATTGGT TGAAATGGAA ATCCGTGACC TATTGTCAGA	180
ATACGACTTC CCAGGTGACG ATCTTCCAGT TATCCAAGGT TCAGCACTTA AAGCTCTTGA	240
AGGTGACTCT AAATACGAAG ACATCGTTAT GGAATTGATG AACACAGTTG ATGAGTATAT	300
CCCAGAACCA GAACGTGACA CTGACAAACC ATTGCTTCTT CCAGTCGAGG ACGTATTCTC	360
AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC CGTGGTATCG TTAAAGTCAA	420
CGACGAAATC GAAATCGTTG GTATCAAAGA AGAACTCRA AAAGCAGTTG TTACTGGTGT	480
TGAAATGTTT CGTAAACAAC TTGACGAAGG TCTTGCTGGA GATAACGTAG GTGTCCTTCT	540
TCGTGGTGTT CAACGTGATG AAATCGAACG TGGACAAGTT ATCGCTAAAC CAGGTTCAAT	600
CAACCCACAC ACTAAATTCA AAGGTGAAGT CTACATCCTT ACTAAAGAAG AAGGTGGACG	660
TCACACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC TTCCGTACTA CTGACGTTAC	720
AGGTTCAATC GAACTTCCAG CAGGTACTGA AATGGTAATG CCTGGTGATA ACGTGACAAT	780
CGACGTTGAG TTGATTCACC CAATCGCCGT AGAACAA	817

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid

- 134 -

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus salivarius*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

CGGTGCGATC CTTGTAGTAG CATCTACTGA CGGACCAATG CCACAAACTC GTGAGCACAT	60
CCTTCTTTCA CGTCAGGTTG GTGTTAAACA CCTTATCGTC TTCATGAACA AAGTTGACTT	120
GGTTGACGAT GAAGAATTGC TTGAATTGGT TGAAATGGAA ATCCGTGACC TTCTTTCAGA	180
ATACGATTTT CCAGGTGATG ACATTCCAGT TATCCAAGGT TCAGCTCTTA AAGCTCTTGA	240
AGGTGATTCT AAATACGAAG ACATCATCAT GGAATTGATG AACACTGTTG ACGAATACAT	300
CCCAGAACCA GAACGTGACA CTGACAAACC ATTGTTGCTT CCAGTCGAAG ACGTATTCTC	360
AATCACTGGT CGTGGTACTG TTGCTTCAGG ACGTATCGAC CGTGGTGTTG TTCGTGTCAA	420
TGACGAAGTT GAAATCGTTG GTCTTAAAGA AGACATCCAA AAAGCAGTTG TTACTGGTGT	480
TGAAATGTTT CGTAAACAAC TTGACGRAGG TATTGCCGGA GATAACGTCG GTGTTCTTCT	540
TCGTGGTATC CAACGTGATG AAATCGAACG TGGTCAAGTA TTGGCTGCAC CTGGTTCAAT	600
CAACCCACAC ACTAAATTCA AAGGTGAAGT TTACATCCTT TCTAAAGAAG AAGGTGGACG	660
TCACACTCCA TTCTTCAACA ACTACCGTCC ACAGTTCTAC TTCCGTACAA CTGACGTAAC	720
AGGTTCAATC GAACTTCCTG CAGGTACTGA AATGGTTATG CCTGGTGATA ACGTGACTAT	780
CGACGTTGAG TTGATCCACC CAATCGCCGT TGAACAA	817

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Agrobacterium tumefaciens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

AACATGATCA CCGGTGCTGC CGAGATGGAC GGC GCGATCC TGGTTTGCTC GGCTGCCGAC	60
GGCCCGATGC CACAGACCCG CGAGCACATC CTGCTTGCCC GTCAGGTGGG CGTTCCGGCC	120

- 135 -

ATCGTCGTGT TCCTCAACAA GGTGACCAG GTTGACGACG CCGAGCTTCT CGAGCTCGTC	180
GAGCTTGAAG TTCGCGAACT TCTGTCGTCC TACGACTTCC CGGGCGACGA TATCCCAGTC	240
ATCAAGGGTT CGGCACTTGC TGCTCTTGAA GATTCTGACA AGAAGATCGG TGAAGACGCG	300
ATCCGCGAGC TGATGGCTGC TGTCGACGCC TACATCCCGA CGCCTGAGCG TCCGATCGAC	360
CAGCCGTTCC TGATGCCGAT CGAAGACGTG TTCTCGATCT CGGGTCGTGG TACGGTTGTG	420
ACGGGTCGCG TTGAGCGCGG TATCGTCAAG GTTGGTGAAG AAGTCGAAAT CGTCGGCATC	480
CGTCCGACCT CGAAGACGAC TGTTACCGGC GTTGAAATGT TCCGCAAGCT GCTCGACCAG	540
GGCCAGGCCG GCGACAACAT CGGTGCACTC GTTCGCGGCG TTACCCGTGA CGGCGTCGAG	600
CGTGGTCAGA TCCTGTGCAA GCCGGGTTTCG GTCAAGCCGC ACAAGAAGTT CATGGCAGAA	660
GCCTACATCC TGACGAAGGA AGAAGGCGGC CGTCATACGC CGTTCTTCAC GAACTACCGT	720
CCGCAGTTCT ACTTCCGTAC GACTGACGTT ACCGGTATCG TTTCGCTTCC TGAAGGCACG	780
GAAATGGTTA TGCCTGGCGA CAACGTCACCT GTTGAAGTCG AGCTGATCGT TCCGATCGCG	840
ATGGAAGAAA AGCTGCGCTT CGCTATCCGC GAAGGCGGCC GTACCGTCGG CGCCGGC	897

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus subtilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

ATGATCACTG GTGCTGCGCA AATGGACGGA GCTATCCTTG TAGTATCTGC TGCTGATGGC	60
CCAATGCCAC AAACCTCGTGA GCACATCCTT CTTTCTAAAA ACGTTGGTGT ACCATACATC	120
GTTGTATTCT TAAACAAATG CGACATGGTA GACGACGAAG AGCTTCTTGA ACTAGTTGAA	180
ATGGAAGTTC GCGATCTTCT TAGCGAATAC GACTTCCCTG GTGATGATGT ACCAGTTGTT	240
AAAGGTTCTG CTCTTAAAGC TCTTGAAGGA GACGCTGAGT GGGAAGCTAA AATCTTCGAA	300
CTTATGGATG CGGTTGATGA GTACATCCCA ACTCCAGAAC GCGACACTGA AAAACCATTC	360
ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACAGTTGC TACTGGCCGT	420
GTAGAACGCG GACAAGTTAA AGTCGGTGAC GAAGTTGAAA TCATCGGTCT TCAAGAAGAG	480

- 136 -

```

AACAAGAAAA CAACTGTTAC AGGTGTTGAA ATGTTCCGTA AGCTTCTTGA TTACGCTGAA      540
GCTGGTGACA ACATTGGTGC CCTTCTTCGC GGTGTATCTC GTGAAGAAAT CCAACGTGGT      600
CAAGTACTTG CTAAACCAGG TACAATCACT CCACACAGCA AATTCAAAGC TGAAGTTTAC      660
GTTCTTTTCTA AAGAAGAGGG TGGACGTCAT ACTCCATTCT TCTCTAACTA CCGTCCTCAG      720
TTCTACTTCC GTACAACTGA CGTAACTGGT ATCATCCATC TTCCAGAAGG CGTAGAAATG      780
GTTATGCCTG GAGATAACAC TGAAATGAAC GTTGAACTTA TTTCTACAAT CGCTATCGAA      840
GAAGGAACTC GTTCTCTAT TCGTGAAGGC GGACGTACTG TTGGT                        885

```

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides fragilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```

ATGGTTACTG GTGCTGCTCA GATGGACGGT GCTATCATTG TAGTTGCTGC TACTGATGGT      60
CCGATGCCTC AGACTCGTGA GCACATCCTT TTGGCTCGTC AGGTAAACGT TCCGAAGCTG      120
GTTGTATTCA TGAACAAAGT CGATATGGTT GAAGATGCTG AGATGTTGGA ACTTGTTGAA      180
ATGGAAATGA GAGAATTGCT TTCATTCTAT GATTTGACG GTGACAATAC TCCGATCATT      240
CAGGGTTCTG CTCTTGGTGC ATTGAACGGC GTAGAAAAAT GGGAAGACAA AGTAATGGAA      300
CTGATGGAAG CTGTTGATAC TTGGATTCCA CTGCCTCCGC GCGATGTTGA TAAACCTTTC      360
TTGATGCCGG TAGAAGACGT GTTCTCTATC ACAGGTCGTG GTACTGTAGC TACAGGTCGT      420
ATCGAAACTG GTGTTATCCA TGTAGGTGAT GAAATCGAAA TCCTCGGTTT GGGTGAAGAT      480
AAGAAATCAG TTGTAACAGG TGTGAAATG TTCCGCAAAC TTCTGGATCA GGGTGAAGCT      540
GGTGACAACG TAGGTCTGTT GCTTCGTGGT GTTGACAAGA ACGAAATCAA ACGTGGTATG      600
GTTCTTTGTA AACCGGGTCA GATTAAACCT CACTCTAAAT TCAAAGCAGA GGTTTATATC      660
CTGAAGAAAG AAGAAGGTGG TCGTCACACT CCATTCCATA ACAAATATCG TCCTCAGTTC      720
TACCTGCGTA CTATGGACTG TACAGGTGAA ATCACTCTTC CGGAAGGAAC TGAAATGGTA      780
ATGCCGGGTG ATAACGTAAC TATCACTGTA GAGTTGATCT ATCCGGTTGC ACTGAACATC      840

```

- 137 -

GGTCTTCGTT TCGCTATCCG CGAAGGTGGA CGTACAGTAG GT

882

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

AATATGATTA CAGGAGCAGC TCAAATGGAT GCAGCGATAC TTTTAGTTGC TGCTGATAGT	60
GGTGCTGAGC CTCAAACAAA AGAGCATTTG CTTCTTGCTC AAAGAATGGG AATAAAGAAA	120
ATAATAGTTT TTTTAAATAA ATTGGACTTA GCAGATCCTG AACTTGTTGA GCTTGTTGAA	180
GTTGAAGTTT TAGAACTTGT TGAAAAATAT GGCTTTTCAG CTGATACTCC AATAATCAAA	240
GGTTCAGCTT TTGGGGCTAT GTCAAATCCA GAAGATCCTG AATCTACAAA ATGCGTTAAA	300
GAACCTCTTG AATCTATGGA TAATTATTTT GATCTTCCAG AAAGAGATAT TGACAAGCCA	360
TTTTTGCTTG CTGTTGAAGA TGTATTTTCT ATTTTCAGGAA GAGGCACTGT TGCTACTGGG	420
CGTATTGAAA GAGGTATTAT TAAAGTTGGT CAAGAAGTTG AAATAGTTGG AATTAAAGAA	480
ACCAGAAAAA CTACTGTTAC TGGTGTGTA ATGTTCCAGA AAATCTTGA GCAAGGTCAA	540
GCAGGGGATA ATGTTGGTCT TCTTTTGAGA GCGTTGATA AAAAAGACAT TGAGAGGGGG	600
CAAGTTTTGT CAGCTCCAGG TACAATTACT CCACACAAGA AATTTAAAGC TTCAATTTAT	660
TGTTTGACTA AAGAAGAAGG CGGTAGGCAC AAGCCATTTT TCCCAGGGTA TAGACCACAG	720
TTCTTTTTTA GAACAACCGA TGTTACTGGA GTTGTTGCTT TAGAGGGCAA AGAAATGGTT	780
ATGCCTGGTG ATAATGTTGA TATTATTGTT GAGCTGATCT CTTCAATAGC TATGGATAAG	840
AATGTAGAAT TTGCTGTTTC AGAAGGTGGA AGAACCGTTG CTTCAGGA	888

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 138 -

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Brevibacterium linens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

AACATGATCA CCGGTGCCGC TCAGATGGAC GGTGCGATCC TCGTCGTCGC CGCTACCGAC	60
GGACCGATGC CCCAGACCCG TGAGCACGTG CTGCTCGCGC GTCAGGTCGG CGTTCCCTAC	120
ATCGTCGTGG CTCTGAACAA GTCCGACATG GTCGATGACG AGGAGCTCCT CGAGCTCGTC	180
GAATTCGAGG TCCGCGACCT GCTCTCGAGC CAGGACTTCG ACGGAGACAA CGCTCCGGTC	240
ATTCCGGTGT CCGCTCTCAA GCGCTGGAA GCGGACGAGA AGTGGGTCAA GAGCGTTCAG	300
GATCTCATGG CTGCCGTCGA TGACAACGTT CCGGAGCCGG AGCGCGATGT CGACAAGCCG	360
TTCCTCATGC CCGTCGAGGA CGTCTTCACG ATCACC GGTC GTGGAACCGT CGTCACCGGT	420
CGTGTGAGC GCGGCGTGCT CCTGCCTAAC GACGAAATCG AAATCGTCGG CATCAAGGAG	480
AAGTCGTCCA AGACGACTGT CACCGCTATC GAGATGTTCC GCAAGACCCT GCCGGATGCC	540
CGTGCAAGTG AGAACGTCGG TCTGCTCCTC CGCGGCACCA AGCGCGAGGA TGTTGAGCGC	600
GGTCAGGTCA TCGTGAAGCC GGGTTCGATC ACCCGCACCA CCAAGTTCGA GGCTCAGGTC	660
TACATCCTGA GCAAGGACGA GGGCGGACGT CACAACCCGT TCTACTCGAA CTACCGTCCG	720
CAGTTCTACT TCCGGACCAC GGACGTCACC GGTGTCATCA CGCTGCCCCA GGGCACCAG	780
ATGGTCATGC CCGGCGACAA CACCGATATG TCGGTCGAGC TCATCCAGCC GATCGCTATG	840
GAGGACCGCC TCCGCTTCGC AATCCGCGAA GGTGGCCGCA CCGTCGGCGC CGGT	894

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Burkholderia cepacia*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

ATGATCACGG GCGCAGCGCA GATGGACGGC GCGATCCTGG TTTGCTCGGC AGCAGACGGC	60
CCGATGCCGC AAACGCGTGA GCACATCCTG CTGGCGCGTC AGGTTGGTGT TCCGTACATC	120
ATCGTGTTC TGAACAAGTG CGACAGTGTG GACGACGCTG AACTGCTCGA GCTGGTTCGAG	180

- 139 -

ATGGAAGTTC GCGAACTCCT GTCGAAGTAC GACTTCCCCG GCGACGACAC GCCGATCGTG	240
AAGGGTTTCG CCAAGCTGGC GCTGGAAGGC GACACGGGCG AGCTGGGCGA AGTGGCGATC	300
ATGAGCCTGG CAGACGCGCT GGACACGTAC ATCCCGACGC CGGAGCGTGC AGTTGACGGC	360
GCGTTCCTGA TGCCGGTGGG AGACGTGTTC TCGATCTCGG GCCGTGGTAC GGTGGTGACG	420
GGTCGTGTCT AGCGCGGCAT CGTGAAGGTC GGCGAAGAAA TCGAAATCGT CGGTATCAAG	480
CCGACGGTGA AGACGACCTG CACGGGCGTT GAAATGTTCC GCAAGCTGCT GGACCAAGGT	540
CAGGCAGGCG ACAACGTCGG TATCCTGCTG CGCGGCACGA AGCGTGAAGA CGTGGAGCGT	600
GGCCAGGTTT TGGCGAAGCC GGGTTCGATC ACGCCGCACA CGCACTTCAC GGCTGAAGTG	660
TACGTGCTGA GCAAGGACGA AGGCGGCCGT CACACGCCGT TCTTCAACAA CTACCGTCCG	720
CAGTTCTACT TCCGTACGAC GGACGTGACG GGCTCGATCG AGCTGCCGAA GGACAAGGAA	780
ATGGTGATGC CGGGCGACAA CGTGTCGATC ACGGTGAAGC TGATTGCTCC GATCGCGATG	840
GAAGAAGGTC TGCGCTTCGC AATCCGTGAA GGCGGCCGTA CGGTCGGC	888

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia trachomatis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

AACATGATCA CCGGTGCGGC TCAAATGGAC GGGGCTATTC TAGTAGTTTC TGCAACAGAC	60
GGAGCTATGC CTCAAATAA AGAGCATATT CTTTGGCAA GACAAGTTGG GGTTCCTTAC	120
ATCGTTGTTT TTCTCAATAA AATTGACATG ATTTCCGAAG AAGACGCTGA ATTGGTCGAC	180
TTGGTTGAGA TGGAGTTGGC TGAGCTTCTT GAAGAGAAAG GATACAAAGG GTGTCCAATC	240
ATCAGAGGTT CTGCTCTGAA AGCTTTGGAA GGAGATGCTG CATAATAGA GAAAGTTCTGA	300
GAGCTAATGC AAGCCGTCGA TGATAATATC CCTACTCCAG AAAGAGAAAT TGACAAGCCT	360
TTCTTAATGC CTATTGAGGA CGTGTTCTCT ATCTCCGAC GAGGAACTGT AGTAACTGGA	420
CGTATTGAGC GTGGAATTGT TAAAGTTTCC GATAAAGTTC AGTTGGTCGG TCTTAGAGAT	480
ACTAAAGAAA CGATTGTTAC TGGGGTTGAA ATGTTTCAGAA AAGAACTCCC AGAAGGTCGT	540

- 140 -

GCAGGAGAGA ACGTTGGATT GCTCCTCAGA GGTATTGGTA AGAACGATGT GGAAAGAGGA	600
ATGGTTGTTT GCTTGCCAAA CAGTGTTAAA CCTCATACAC AGTTTAAGTG TGCTGTTTAC	660
GTTCTGCAAA AAGAAGAAGG TGGACGACAT AAGCCTTTCT TCACAGGATA TAGACCTCAA	720
TTCTTCTTCC GTACAACAGA CGTTACAGGT GTGGTAACTC TGCCTGAGGG AGTTGAGATG	780
GTCATGCCTG GGGATAACGT TGAGTTTGAA GTGCAATTGA TTAGCCCTGT GGCTTTAGAA	840
GAAGGTATGA GATTTGCGAT TCGTGAAGGT GGTCGTACAA TCGGTGCTGG A	891

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

AACATGATCA CCGGTGCTGC GCAGATGGAC GCGCGATCC TGGTAGTTGC TGCGACTGAC	60
GGCCCGATGC CGCAGACTCG TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC	120
ATCATCGTGT TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAC TG GTT	180
GAAATGGAAG TTCGTGAAC TCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC	240
GTCGTGGT CTGCTCTGAA AGCGCTGGAA GCGGACGCAG AGTGGGAAGC GAAAATCCTG	300
GAACTGGCTG GCTTCCTGGA TTCTTACATT CCGGAACCAG AGCGTGCGAT TGACAAGCCG	360
TTCTTGCTGC CGATCGAAGA CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT	420
CGTG TAGAAC GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG	480
ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT	540
GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT CGAACGTGGT	600
CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA AGTTCGAATC TGAAGTGATC	660
ATTCTGTCCA AAGATGAAGG CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG	720
TTCTACTTCC GTACTACTGA CGTGA CTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG	780
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCGATGGAC	840
GACGGTCTGC GTTTCGCAAT CCGTGAAGGC GGCCGTACCG TTGGCGCGGG C	891

- 141 -

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fibrobacter succinogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

AACATGGTGA CTGGTGCTGC TCAGATGGAC GGCGCTATCC TCGTTGTTGC CGCTACTGAC	60
GGTCCGATGC CGCAGACTCG CGAACACATC CTTCTCGCTC ACCAGGTTGG CGTGCCGAAG	120
ATCGTCGTGT TCATGAACAA GTGCGACATG GTTGACGATG CTGAAATTCT CGACCTCGTC	180
GAAATGGAAG TTCGCGAACT CCTCTCCAAG TATGACTTCG ACGGTGACAA CACCCCGATC	240
ATCCGTGGTT CCGCTCTCAA GGCCCTCGAA GGCGATCCGG AATACCAGGA CAAGGTCATG	300
GAACTCATGA ACGCTTGCGA CGAATACATC CCGTCCCCGC AGCGCGATAC CGACAAGCCG	360
TTCTCATGC CGATCGAAGA CGTGTTACG ATTACTGGCC GCGGCACTGT CGCTACTGGC	420
CGTATCGAAC GCGGTGTCGT TCGCTTGAAC GACAAGGTTG AACGTATCGG TCTCGGTGAA	480
ACCACCGAAT ACGTCATCAC CCGTGTTGAA ATGTTCCGTA AGCTCCTCGA CGACGCTCAG	540
GCAGGTGACA ACGTTGGTCT CCTCCTCCGT GGTGCTGAAA AGAAGGACAT CGTCCGTGGC	600
ATGGTTCTCG CAGCTCCGAA GTCTGTCACT CCGCACACCG AATTTAAGGC TGAAATCTAC	660
GTTCTCACGA AGGACGAAGG TGGCCGTCAC ACGCCGTTCA TGAATGGCTA CCGTCCGCAG	720
TTCTACTTCC GCACCACCGA CGTTACTGGT ACGATCCAGC TCCCGGAAGG TGTCGAAATG	780
GTTACTCCGG GTGACACGGT CACGATCCAC GTGAACCTCA TCGCTCCGAT CGCTATGGAA	840
AAGCAGCTCC GCTTCGCTAT CCGTGAAGGT GGACGTACTG TTGGTGCTGG C	891

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 142 -

(A) ORGANISM: *Flavobacterium ferrugineum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

AACATGATCA CCGGTGCTGC CCAGATGGAC GGTGCTATCT TAGTTGTGGC TGCATCAGAC	60
GGTCCTATGC CTCAAACAAA AGAACACATC CTGCTTGCTG CCCAGGTAGG TGTACCTAAA	120
ATGGTTGTGT TTCTGAATAA AGTTGACCTC GTTGACGACG AAGAGCTCCT GGAGCTGGTT	180
GAGATCGAGG TTCGCGAAGA ACTGACTAAA CGCGGTTTCG ACGGCGACAA CACTCCAATC	240
ATCAAAGGTT CCGCTACAGG CGCCCTCGCT GGTGAAGAAA AGTGGGTAA AGAAATTGAA	300
AACCTGATGG ACGCTGTTGA CAGCTACATC CCACTGCCTC CTCGTCCGGT TGATCTGCCG	360
TTCCTGATGA GCGTAGAGGA CGTATTCTCT ATCACTGGTC GTGGTACTGT TGCTACCGGT	420
CGTATCGAGC GTGGCCGTAT CAAAGTTGGT GAGCCTGTTG AGATCGTAGG TCTGCAGGAG	480
TCTCCCCTGA ACTCTACCGT TACAGGTGTT GAGATGTTCC GCAAACCTCT CGACGAAGGT	540
GAAGCTGGTG ATAACGCCGG TCTCCTCCTC CGTGGTGTG AAAAAACACA GATCCGTCGC	600
GGTATGGTAA TCGTTAAACC CGGTTCCATC ACTCCGCACA CGGACTTCAA AGGCGAAGTT	660
TACGTACTGA GCAAAGACGA AGGTGGCCGT CACACTCCAT TCTTCAACAA ATACCGTCCT	720
CAATTCTACT TCCGTACAAC TGACGTTACA GGTGAAGTAG AACTGAACGC AGGAACAGAA	780
ATGGTTATGC CTGGTGATAA CACCAACCTG ACCGTTAAAC TGATCCAACC GATCGCTATG	840
GAAAAGGTC TGAAATTCGC GATCCGCGAA GGTGGCCGTA CCGTAGGTGC AGGA	894

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

AATATGATTA CTGGTGCGGC ACAAATGGAT GGTGCTATTT TAGTAGTAGC AGCAACAGAT	60
GGTCCTATGC CACAACTCG TGAACACATC TTATTAGGTC GCCAAGTAGG TGTTCCATAC	120
ATCATCGTAT TCTTAAACAA ATGCGACATG GTAGATGACG AAGAGTTATT AGAATTAGTC	180
GAAATGGAAG TTCGTGAACT TCTATCTCAA TATGACTTCC CAGGTGACGA TACACCAATC	240

- 143 -

GTACGTGGTT CAGCATTACA AGCGTTAAAC GCGTAGCAG AATGGGAAGA AAAAATCCTT	300
GAGTTAGCAA ACCACTTAGA TACTTACATC CCAGAACCAG AACGTGCGAT TGACCAACCG	360
TTCCTTCTTC CAATCGAAGA TGTGTTCTCA ATCTCAGGTC GTGGTACTGT AGTAACAGGT	420
CGTGTAGAAC GAGGTATTAT CCGTACAGGT GATGAAGTAG AAATCGTCGG TATCAAAGAT	480
ACAGCGAAAA CTACTGTAAC GGGTGTGAA ATGTTCCGTA AATTACTTGA CGAAGGTCGT	540
GCAGGTGAAA ACATCGGTGC ATTATTACGT GGTACCAAAC GTGAAGAAAT CGAACGTGGT	600
CAAGTATTAG CGAAACCAGG TTCAATCACA CCACACACTG ACTTCGAATC AGAAGTGTAC	660
GTATTATCAA AAGATGAAGG TGGTCGTCAT ACTCCATTCT TCAAAGGTTA CCGTCCACAA	720
TTCTATTTCC GTACAACAGA CGTGACTGGT ACAATCGAAT TACCAGAAGG CGTGGAATG	780
GTAATGCCAG GCGATAACAT CAAGATGACA GTAAGCTTAA TCCACCCAAT TGCGATGGAT	840
CAAGGTTTAC GTTTCGCAAT CCGTGAAGGT GGCCGTACAG TAGGTGCAGG C	891

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

AACATGATCA CCGGTGCGGC GCAAATGGAC GGAGCGATTT TGGTTGTTTC TGCAGCTGAT	60
GGCCCTATGC CTCAAAC TAG GGAGCATATC TTATTGTCTC GTCAAGTAGG CGTGCCTCAC	120
ATCGTTGTTT TCTTAAACAA ACAAGACATG GTAGATGACC AAGAATTGTT AGAACTTGTA	180
GAAATGGAAG TGCGCGAATT GTTGAGCGCG TATGAATTTT CTGGCGATGA CACTCCTATC	240
GTAGCGGGTT CAGCTTTAAG AGCTTTAGAA GAAGCAAAGG CTGGTAATGT GGGTGAATGG	300
GGTGAAAAAG TGCTTAAACT TATGGCTGAA GTGGATGCCT ATATCCCTAC TCCAGAAAGA	360
GACACTGAAA AAACCTTCTT GATGCCGGTT GAAGATGTGT TCTCTATTGC GGGTAGAGGG	420
ACTGTGGTTA CAGGTAGGAT TGAAAGAGGC GTGGTGAAAG TAGGCGATGA AGTGGAATC	480
GTTGGTATCA GACCTACACA AAAACGACT GTAACCGGTG TAGAAATGTT TAGGAAAGAG	540
TTGGA AAAAG GTGAAGCCGG CGATAATGTG GCGGTGCTTT TGAGAGGAAC TAAAAAAGAA	600

- 144 -

GAAGTGGAAC GCGGTATGGT TCTATGCAAA CCAGGTTCTA TCACTCCGCA CAAGAAATTT	660
GAGGGAGAAA TTTATGTCCT TTCTAAAGAA GAAGGCGGGA GACACACTCC ATTCTTCACC	720
AATTACCGCC CGCAATTCTA TGTGCGCACA ACTGATGTGA CTGGCTCTAT CACCCTTCCT	780
GAAGGCGTAG AAATGGTTAT GCCTGGCGAT AATGTGAAAA TCACTGTAGA GTTGATTAGC	840
CCTGTTGCGT TAGAGTTGGG AACTAAATTT GCGATTCGTG AAGGCGGTAG GACCGTTGGT	900
GCTGGT	906

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Micrococcus luteus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

AACATGATCA CCGGCGCCGC TCAGATGGAC GGC GCGATCC TCGTGGTCGC CGCTACCGAC	60
GGCCCGATGG CCCAGACCCG TGAGCACGTG CTCCTGGCCC GCCAGGTCGG CGTGCCGGCC	120
CTGCTCGTGG CCCTGAACAA GTCGGACATG GTGGAGGACG AGGAGCTCCT CGAGCGTGTC	180
GAGATGGAGG TCCGGCAGCT GCTGTCCTCC AGGAGCTTCG ACGTCGACGA GGCCCCGGTC	240
ATCCGCACCT CCGCTCTGAA GGCCCTCGAG GGC GACCCCC AGTGGGTCAA GTCCGTCGAG	300
GACCTCATGG ATGCCGTGGA CGAGTACATC CCGGACCCGG TCGCGACAA GGACAAGCCG	360
TTCCTGATGC CGATCGAGGA CGTCTTCACG ATCACC GGCC GTGGCACCGT GGTGACCGGT	420
CGCGCCGAGC GCGGCACCCCT GAAGATCAAC TCCGAGGTCG AGATCGTCGG CATCCGCGAC	480
GTGCAGAAGA CCACTGTCAC CGGCATCGAG ATGTTCCACA AGCAGCTCGA CGAGGCCTGG	540
GCCGGCGAGA ACTGCGGTCT GCTCGTGCGC GGTCTGAAGC GCGACGACGT CGAGCGCGGC	600
CAGGTGCTGG TGGAGCCGGG CTCCATCACC CCGCACACCA ACTTCGAGGC GAACGTCTAC	660
ATCCTGTCCA AGGACGAGGG TGGGCGTCAC ACCCGTTCT ACTCGAACTA CCGCGCGCAG	720
TTCTACTTCC GCACCACCGA CGTCACCGGC GTCATCACGC TGCCCGAGGG CACCGAGATG	780
GTCATGCCCC GCGACACCAC CGAGATGTCG GTCGAGCTCA TCCAGCCGAT CGCCATGGAG	840
GAGGGCCTCG GCTTCGCCAT CCGCGAGGGT GGCCGCACCG TGGGCTCCGG C	891

- 145 -

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```

AACATGATCA CCGGCGCCGC GCAGATGGAC GGTGCGATCC TGGTGGTCGC CGCCACCGAC      60
GGCCCCGATGC CCCAGACCCG CGAGCACGTT CTGCTGGCGC GTCAAGTGGG TGTGCCCTAC      120
ATCCTGGTAG CGCTGAACAA GGCCGACGCA GTGGACGACG AGGAGCTGCT CGAACTCGTC      180
GAGATGGAGG TCCGCGAGCT GCTGGCTGCC CAGGAATTCTG ACGAGGACGC CCCGGTTGTG      240
CGGGTCTCGG CGCTCAAGGC GCTCGAGGGT GACGCGAAGT GGGTTGCCTC TGTCGAGGAA      300
CTGATGAACG CGGTGACGA GTCGATTCCG GACCCGGTCC GCGAGACCGA CAAGCCGTTC      360
CTGATGCCGG TCGAGGACGT CTTACCATT ACCGGCCGCG GAACCGTGGT CACCGGACGT      420
GTGGAGCGCG GCGTGATCAA CGTGAACGAG GAAGTTGAGA TCGTCGGCAT TCGCCCATCG      480
ACCACCAAGA CCACCGTCAC CGGTGTGGAG ATGTTCCGCA AGCTGCTCGA CCAGGGCCAG      540
GCGGGCGACA ACGTTGGTTT GCTGCTGCGG GCGCTCAAGC GCGAGGACGT CGAGCGTGCG      600
CAGGTTGTCA CCAAGCCCGG CACCACCACG CCGCACACCG AGTTCGAAGG CCAGGTCTAC      660
ATCCTGTCCA AGGACGAGGG CGGCCGGCAC ACGCCGTTCT TCAACAATA CCGTCCGCAG      720
TTCTACTTCC GCACCACCGA CGTGACCGGT GTGGTGACAC TGCCGGAGGG CACCGAGATG      780
GTGATGCCCC GTGACAACAC CAACATCTCG GTGAAGTTGA TCCAGCCCGT CGCCATGGAC      840
GAAGGTCTGC GTTTCGCGAT CCGCGAGGGT GGCCGCACCG TGGGCGCCGG C      891

```

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 146 -

(A) ORGANISM: *Mycoplasma genitalium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

AATATGATCA CAGGTGCTGC ACAAATGGAT GGAGCTATTC TAGTTGTTTC AGCAACTGAT	60
AGTGTGATGC CCCAAACCCG CGAGCACATC TTACTTGCCC GCCAAGTAGG GGTTCCTAAA	120
ATGGTAGTTT TTCTAAACAA GTGTGATATT GCTAGTGATG AAGAGGTACA AGAACTTGTT	180
GCTGAAGAAG TACGTGATCT GTTAACCTCC TATGGTTTTG ATGGTAAGAA CACTCCTATT	240
ATTTATGGCT CAGCTTTAAA AGCATTGGAA GGTGATCCAA AGTGGGAGGC TAAGATCCAT	300
GATTTGATTA AAGCAGTTGA TGAATGGATT CCAACTCCTA CACGTGAAGT AGATAAACCT	360
TTCTTATTAG CAATTGAAGA TACGATGACC ATTACTGGTA GAGGTACAGT TGTTACAGGA	420
AGAGTTGAAA GAGGTGAACT CAAAGTAGGT CAAGAAGTTG AAATTGTTGG TTTAAAACCA	480
ATTAGAAAAG CAGTTGTTAC TGGAATTGAA ATGTTCAAAA AGGAACTTGA TTCAGCAATG	540
GCTGGTGACA ATGCTGGGGT ATTATTACGT GGTGTTGAAC GTAAAGAAGT TGAAAGAGGT	600
CAAGTTTTAG CAAAACCAGG CTCTATTAAA CCGCACAAGA AATTTAAAGC TGAGATCTAT	660
GCTTTAAAGA AAGAAGAAGG TGGTAGACAC ACTGGTTTTT TAAACGGTTA CCGTCCTCAA	720
TTCTATTTCC GTACCACTGA TGTAACGGT TCTATTGCTT TAGCTGAAAA TACTGAAATG	780
GTTCTACCTG GTGATAATGC TTCTATTACT GTTGAGTTAA TTGCTCCTAT CGCTTGTAAG	840
AAAGGTAGTA AGTTCTCAAT TCGTGAAGGT GGTAGAACTG TAGGGGCAGG C	891

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

AACATGATTA CCGGCGCCGC ACAAATGGAC GGTGCAATCC TGGTATGTTT TGCTGCCGAC	60
GGCCCTATGC CGCAAACCCG CGAACACATC CTGCTGGCCC GTCAAGTAGG CGTACCTTAC	120
ATCATCGTGT TCATGAACAA ATGCGACATG GTCGACGATG CCGAGCTGTT CCAACTGGTT	180
GAAATGGAAA TCCGCGACCT GCTGTCCAGC TACGACTTCC CCGGCGACGA CTGCCCGATC	240

- 147 -

GTACAAGGTT	CCGCACTGAA	AGCCTTGGAA	GGCGATGCCG	CTTACGAAGA	AAAAATCTTC	300
GAACTGGCTA	CCGCATTGGA	CAGATACATC	CCGACTCCCG	AGCGTGCCGT	GGACAAACCA	360
TTCTTGCTGC	CTATCGAAGA	CGTGTTCTCC	ATTTCCGGCC	GCGGTACCGT	AGTCACCGGC	420
CGTGTAAGAGC	GAGGTATCAT	CCACGTTGGT	GACGAGATTG	AAATCGTCGG	TCTGAAAGAA	480
ACCCAAAAAA	CCACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGTCAG	540
GCGGGCGACA	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	GTGAAGACGT	AGAACGCGGT	600
CAGGTATTGG	CCAAACGGGG	TACTATCACT	CCTCACACCA	AGTTCAAAGC	AGAAGTGTAC	660
GTATTGAGCA	AAGAAGAGGG	CGGCCCCCAT	ACCCCGTTTT	TCGCCAACTA	CCGTCCCCAA	720
TTCTACTTCC	GTACCACTGA	CGTAACCGGC	ACGATTACTT	TGGAAAAAGG	TGTGGAAATG	780
GTAATGCCGG	GTGAGAACGT	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	CGCTATGGAA	840
GAAGGTCTGC	GCTTTGCGAT	TCGCGAAGGC	GGCCGTACCG	TGGGTGCCGG	C	891

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rickettsia prowazekii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

AATATGATAA	CTGGTGCCGC	TCAGATGGAT	GGTGCTATAT	TAGTAGTTTC	TGCTGCTGAT	60
GGTCCTATGC	CTCAAAC TAG	AGAACATATA	TTACTGGCAA	AACAGGTAGG	TGTACCTGCT	120
ATGGTAGTAT	TTTTGAATAA	AGTAGATATG	G TAGATGATC	CTGACCTATT	AGAATTAGTT	180
GAGATGGAAG	TAAGAGAATT	ATTATCAAAA	TATGGTTTCC	CTGGTAATGA	AATACCTATT	240
ATTAAAGGTT	CTGCACTTCA	AGCTTTAGAA	GGAAAACCTG	AAGGTGAAAA	AGCTATTAAAT	300
GAGTTAATGA	ATGCAGTAGA	TACGTATATA	CCTCAGCCTA	TAGAGCTACA	AGATAAACCT	360
TTTTTAATGC	CAATAGAGGA	TGTATTTTCT	ATTTCAGGCA	GAGGTACCGT	TGTAAC TGGT	420
AGAGTGGAGT	CAGGCATAAT	TAAGGTGGGT	GAAGAAAATTG	AAATAGTAGG	TCTAAAAAAT	480
ACGCAAAAAA	C GACTTG TAC	AGGTGTAGAA	ATGTT CAGAA	AATTACTTGA	TGAAGGACAA	540
TCTGGAGATA	ATGTCGGTAT	ATTACTACGT	GGTACAAAAA	GAGAAGAAGT	AGAAAGAGGA	600

- 148 -

CAAGTACTTG CAAAACCTGG GAGCATAAAA CCGCATGATA AATTTGAAGC TGAAGTGTAT	660
GTGCTTAGTA AAGAGGAAGG TGGACGTCAT ACCCCATTTA CTAATGATTA TCGCCACAG	720
TTCTATTTTA GAACAACAGA TGTTACCGGC ACAATAAAAT TGCCTTCTGA TAAGCAGATG	780
GTTATGCCTG GAGATAATGC TACTTTTTTCA GTAGAATTAA TTAAGCCGAT TGCTATGCAA	840
GAAGGGTTAA AATTCTCTAT ACGTGAAGGT GGTAGAACAG TAGGAGCCGG T	891

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

AACATGATCA CCGGTGCTGC TCAGATGGAC GGCGCGATCC TGGTTGTTGC TGCGACTGAC	60
GGCCCGATGC CGCAGACCCG TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC	120
ATCATCGTGT TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT	180
GAGATGGAAG TTCGCGAACT GCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC	240
GTTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC GAAAATCATC	300
GAAGTGGCTG GCTTCCTGGA TTCTTATATT CCGGAACCAG AGCGTGCGAT TGACAAGCCG	360
TTCCTGCTGC CGATCGAAGA CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTACCAGGT	420
CGTGTAGAGC GCGGTATCAT CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG	480
ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT	540
GCCGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT CGAACGTGGT	600
CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA AGTTCGAATC TGAAGTGTAC	660
ATTCTGTCCA AAGATGAAGG CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG	720
TTCTACTTCC GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG	780
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCGATGGAC	840
GACGGTCTGC GTTTCGCAAT CCGTGAAGGC GGCCGTACCG TTGGCGCGGG C	891

(2) INFORMATION FOR SEQ ID NO: 165:

- 149 -

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 881 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putida*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

```

ATGATCACTG GTGCTGCACA GATGGACGGC GCGATTCTGG TAGTCGCTTC AACAGACGGT      60
CCAATGCCAC AGACTCGTGA GCACATCCTG CTTTCTCGTC AGGTTGGCGT ACCATTTCATC      120
ATCGTATTCA TGAACAAATG TGACATGGTA GATGACGAAG AGCTGTTAGA GCTAGTTGAG      180
ATGGAAGTGC GTGAAGTGT ATCAGAATAC GATTTCCAG GTGATGACTT ACCGGTAATC      240
CAAGGTTTCA CTCTGAAAGC GCTAGAAGGC GAGCCAGAGT GGGAAGCAAA AATCCTTGAA      300
TTAGCAGCGG CGCTGGATTC TTACATTCCA GAACCACAAC GTGACATCGA TAAGCCGTTT      360
CTACTGCCAA TCGAAGACGT ATTCTCAATT TCAGGCCGTG GTACAGTAGT AACAGGTCGT      420
GTTGAGCGTG GTATTGTACG CGTAGGCGAC GAAGTTGAAA TCGTTGGTGT ACGTGCGACA      480
ACTAAGACAA CGTGTACTGG TGTAGAAATG TTCCGTAAAC TGCTTGACGA AGGTCGTGCA      540
GGTGAGAACT GTGGTATTTT GTTACGTGGT ACTAAGCGTG ATGACGTAGA ACGTGGTCAA      600
GTATTAGCGA AGCCAGGTTC AATCAACCCA CACTACTT TTGAATCAGA AGTTTACGTA      660
CTGTCAAAAG AAGAAGGTGG TCGTCACACG CCATTCTTCA AAGGCTACCG TCCACAGTTC      720
TACTTCCGTA CAACTGACGT AACCGGTACT ATCGAACTGC CAGAAGGCGT AGAGATGGTA      780
ATGCCAGGCG ATAACATCAA GATGGTAGTG AACTGATTT GCCCAATCGC GATGGACGAA      840
GGTTTACGCT TCGCAATCCG TGAAGGCGGT CGTACAGTGG T                                881

```

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stigmatella aurantiaca*

- 150 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

AACATGATCA	CGGGCGCGGC	GCAGATGGAC	GGAGCGATTC	TGGTGGTGTC	CGCGGCCGAC	60
GGCCCGATGC	CCCAGACGCG	TGAGCACATC	CTGCTGGCCA	GGCAGGTGGG	CGTGCCCTAC	120
ATCGTCGTCT	TCCTGAACAA	GGTGGACATG	CTGGACGATC	CGGAGCTGCG	CGAGCTGGTG	180
GAGATGGAGG	TGCGCGACCT	GCTCAAGAAG	TACGAGTTCC	CGGGCGACAG	CATCCCCATC	240
ATCCCTGGCA	GCGCGCTCAA	GGCGCTGGAG	GGAGACACCA	GCGACATCGG	CGAGGGAGCG	300
ATCCTGAAGC	TGATGGCGGC	GGTGGACGAG	TACATCCCGA	CGCCGCAGCG	TGCGACGGAC	360
AAGCCGTTCC	TGATGCCGGT	GGAAGACGTG	TTCTCCATCG	CAGGCCGAGG	AACGGTGGCG	420
ACGGGCCGAG	TGGAGCGCGG	CAAGATCAAG	GTGGGCGAGG	AAGTGGAGAT	CGTGGGGATC	480
CGTCCGACGC	AGAAGACGGT	CATCACGGGG	GTGGAGATGT	TCCGCAAGCT	GCTGGACGAG	540
GGCATGGCGG	GAGACAACAT	CGGAGCGCTG	CTGCGAGGCC	TGAAGCGCGA	GGACCTGGAG	600
CGTGGGCAGG	TGCTGGCGAA	CTGGGGGAGC	ATCAACCCGC	ACACGAAGTT	CAAGGCGCAG	660
GTGTACGTGC	TGTCGAAGGA	AGAGGGAGGG	CGGCACACGC	CGTTCTTCAA	GGGATAACGG	720
CCGCAGTTCT	ACTTCCGGAC	GACGGACGTG	ACCGGAACGG	TGAAGCTGCC	GGACAACGTG	780
GAGATGGTGA	TGCCGGGAGA	CAACATCGCC	ATCGAGGTGG	AGCTCATTAC	TCCGGTCGCC	840
ATGGAGAAAG	AGCTGCCGTT	CGCCATCCGT	GAGGGTGGCC	GCACGGTGGG	CGCCGGC	897

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

AACATGATCA	CTGGTGCCGC	TCAAATGGAC	GGAGCTATCC	TTGTAGTTGC	TTCAACTGAT	60
GGACCAATGC	CACAACTCG	TGAGCACATC	CTTCTTTCAC	GTCAGGTGG	TGTTAAACAC	120
CTTATCGTGT	TCATGAACAA	AGTTGACCTT	GTTGATGACG	AAGAGTTGCT	TGAATTAGTT	180
GAGATGGAAA	TTCGTGACCT	TCTTTCAGAA	TACGATTTC	CAGGTGATGA	CCTTCCAGTT	240
ATCCAAGGTT	CAGCTCTTAA	AGCTCTTGAA	GGCGACACTA	AATTGAAGA	CATCATCATG	300

- 151 -

GAATTGATGG	ATACTGTTGA	TTCATACATT	CCAGAACCAG	AACGCGACAC	TGACAAACCA	360
TTGCTTCTTC	CAGTCGAAGA	CGTATTCTCA	ATTACAGGTC	GTGGTACAGT	TGCTTCAGGA	420
CGTATCGACC	GTGGTACTGT	TCGTGTCAAC	GACGAAATCG	AAATCGTTGG	TATCAAAGAA	480
GAAACTAAAA	AAGCTGTTGT	TACTGGTGTT	GAAATGTTCC	GTAAACAAC	TGACGAAGGT	540
CTTGCAGGAG	ACAACGTAGG	TATCCTTCTT	CGTGGTGTTT	AACGTGACGA	AATCGAACGT	600
GGTCAAGTTA	TTGCTAAACC	AAGTTCAATC	AACCCACACA	CTAAATTCAA	AGGTGAAGTA	660
TATATCCTTT	CTAAAGACGA	AGGTGGACGT	CACACTCCAT	TCTTCAACAA	CTACCGTCCA	720
CAATTCTACT	TCCGTACAAC	TGACGTAACA	GGTTCAATCG	AACCTCCAGC	AGGTACAGAA	780
ATGGTTATGC	CTGGTGATAA	CGTGACAATC	AACGTTGAGT	TGATCCACCC	AATCGCCGTA	840
GAACAAGGTA	CTACTTTCTC	AATCCGTGAA	GGTGGACGTA	CTGTTGGTTC	AGGT	894

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Thiobacillus cuprinus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

AACATGATCA	CCGGTGCGGC	CCAGATGGAC	GGCGCCATCC	TGGTCGTGTC	CGCCGCCGAC	60
GGCCCCATGC	CCCAAACCCG	CGAGCACATC	CTGCTGGCGC	GTCAGGTGGG	CGTGCCCTAC	120
ATCATCGTGT	TCCTCAACAA	GTGCGACATG	GTCGACGACG	CCGAGCTGCT	CGAACTCGTC	180
GAGATGGAAG	TGCGCGAGCT	GCTGTCCAAG	TACGACTTCC	CCGGTGACGA	CACCCCCATC	240
ATCAAGGGCT	CGGCCAAGCT	GGCCCTCGAA	GGCGACAAGG	GCGAACTGGG	CGAAGGCGCC	300
ATTCTCAAGC	TGGCCGAGGC	CCTGGACACC	TACATCCCCA	CGCCCGAGCG	GGCCGTGCGAC	360
GGCGCGTTCC	TCATGCCCGT	GGAAGACGTG	TTCTCCATCT	CCGGGCGCGG	CACGGTGGTC	420
ACCGGGCGTG	TGGAGCGCGG	CATCATCAAG	GTCGGCGAGG	AAATCGAGAT	TGTCGGCCTC	480
AAGCCCACCC	TCAAGACCAC	CTGCACCGGC	GTGGAAATGT	TCAGGAAGCT	GCTCGACCAG	540
GGCCAGGCCG	GCGACAACGT	CGGCATCTTG	CTGCGCGGCA	CCAAGCGCGA	GGAAGTCGAG	600
CGCGGCCAGG	TGCTGTGCAA	ACCCGGCTCG	ATCAAGCCCC	ACACCCACTT	CACCGCCGAG	660

- 152 -

GTGTACGTGC TGAGCAAGGA CGAGGGCGGC CGCCACACCC CCTTCTTCAA CAACTACCGC	720
CCGCAGTTCT ACTTCCGCAC CACCGACGTC ACCGGCGCCA TCGAACTGCC CAAGGACAAG	780
GAAATGGTCA TGCCCGGCGA TAATGTGAGC ATCACCGTCA AGCTCATCGC CCCCATCGCC	840
ATGGAAGAAG GCCTGCGCTT CGCCATCCGC GAAGGCGGCC GCACCGTCGG CGCCGGC	897

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Treponema pallidum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

AATATGATCA CGGGTGCTGC GCAGATGGAC GGTGGTATTC TCGTCGTGTC TGCGCCTGAC	60
GGCGTTATGC CACAGACGAA GGAGCATCTT CTGCTCGCCC GTCAGGTTGG TGTTCCCTCC	120
ATCATTGTTT TTTTGAACAA GGTGATTG GTTGATGATC CTGAGTTGCT AGAGCTGGTG	180
GAAGAAGAGG TCGTGATGC GCTTGCTGGA TATGGGTTTT CGCGTGAGAC GCCTATCGTC	240
AAGGGGTCTG CGTTTAAAGC TCTGCAGGAT GGCGCTTCCC CGGAGGATGC AGCTTGATTT	300
GAGGAAGTGC TTGCGGCCAT GGATTCCTAC TTTGAAGACC CAGTGCCTGA CGACGCAAGA	360
CCTTTCTTGC TCTCTATCGA GGATGTGTAC ACTATTTCTG GGCCTGGTAC CGTTGTCACG	420
GGGCGCATCG AATGTGGGGT AATTAGTCTG AATGAAGAGG TCGAGATCGT CGGGATTAAG	480
CCCACTAAGA AAACAGTGGT TACTGGCATT GAGATGTTTA ATAAGTTGCT TGATCAGGGA	540
ATTGCAGGTG ATAACGTGGG GCTGCTTTTG CGCGGGGTGG ATAAAAAGA GGTTGAGCGC	600
GGTCAGGTGC TTTCTAAGCC CGGTTCTATT AAGCCACACA CCAAGTTTGA GGCGCAGATC	660
TACGTGCTCT CTAAGGAAGA GGGTGGCCGT CACAGTCCTT TTTTCAAGG TTATCGTCCG	720
CAGTTTTATT TTAGAACTAC TGACATTACC GGTACGATTT CTCTTCCTGA AGGGGTAGAC	780
ATGGTGAAGC CGGGGGATAA CACCAAGATT ATAGGTGAGC TCATCCACCC GATAGCTATG	840
GACAAGGGTC TGAAGCTTGC GATTCGTGAA GGGGGGCGCA CTATTGCTTC TGGT	894

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- 153 -

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Ureaplasma urealyticum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

AATATGATTA CAGGGGCAGC ACAAATGGAT GGAGCAATTT TAGTTATTGC TGCATCTGAT	60
GGGGTTATGG CTCAAACATA AGAACATATT TTATTAGCAC GTCAAGTTGG TGTTCACAAA	120
ATCGTTGTTT TCTTAAACAA ATGTGATTTT ATGACAGATC CAGATATGCA AGATCTTGTT	180
GAAATGGAAG TTCGTGAATT ATTATCTAAA TATGGATTTG ATGGCGATAA CACACCAGTT	240
ATTCGTGGTT CAGGTCTTAA GGCTTTAGAA GGAGATCCAG TTTGAGAAGC AAAAATTGAT	300
GAATTAATGG ACGCAGTTGA TTCATGAATT CCATTACCAG AACGTAGTAC TGACAAACCA	360
TTCTTATTAG CAATTGAAGA TGTATTCACA ATTTTCAGGAC GTGGTACAGT AGTAACTGGA	420
CGTGTTGAAC GTGGTGTATT AAAAGTTAAT GATGAGGTTG AAATTGTTGG TCTAAAAGAC	480
ACTCAAAAAA CTGTTGTTAC AGGAATTGAA ATGTTTAGAA AATCATTAGA TCAAGCTGAA	540
GCTGGTGATA ATGCTGGTAT TTTATTACGT GGTATTAAAA AAGAAGATGT TGAACGTGGT	600
CAAGTACTTG TAAAACCAGG ATCAATTAAA CCTCACCGTA CTTTTACTGC TAAAGTTTAT	660
ATTCTTAAAA AAGAAGAAGG TGGACGTCAT ACACCTATTG TTTCAGGATA CCGTCCACAA	720
TTCTATTTTA GAACAACAGA TGTAACAGGT GCTATTTTCAT TACCTGCTGG TGTTGATTTG	780
GTTATGCCAG GTGATGACGT TGAAATGACT GTAGAATTAA TTGCTCCAGT TGCGATTGAA	840
GATGGATCTA AATTCTCAAT CCGTGAAGGT GGTAAACTG TAGGTCATGG T	891

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 909 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Wolinella succinogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

- 154 -

AACATGATTA CAGGTGCTGC TCAAATGGAT GGCGCGATTC TTGTTGTTTC TCGGCGGAT	60
GGCCCCATGC CCCAACTAG GGAGCACATT CTTCCTTCTC GACAAGTAGG CGTTCCTTAC	120
ATCGTGGTTT TCTTGAACAA AGAAGATATG GTTGATGACG CTGAGCTTCT TGAGCTTGTT	180
GAAATGGAAG TTAGAGAACT TCTTAGCAAC TACGACTTCC CTGGAGATGA CACTCCTATC	240
GTTGCAGGTT CCGCTCTTAA AGCTCTTGAA GAGGCTAACG ACCAGGAAAA TGTTGGCGAG	300
TGGGGCGAGA AAGTATTGAA GCTTATGGCT GAGGTTGACC GATATATTCC TACGCCTGAG	360
CGAGATGTGG ATAAGCCTTT CCTTATGCCT GTTGAAGACG TATTCTCCAT CGCGGGTCGT	420
GGAACCGTTG TGACAGGAAG AATTGAAAGA GGCGTGTTA AAGTCGGTGA CGAAGTAGAA	480
ATCGTTGGTA TCCGAAACAC ACAAAAAACA ACCGTAAGT GCGTTGAGAT GTTCCGAAAA	540
GAGCTCGACA AGGGTGAGGC GGGTGACAAC GTTGGTGTTT TTTTGAGAGG CACCAAGAAA	600
GAAGATGTTG AGAGAGGTAT GGTTCTTTGT AAAATAGGTT CTATCACTCC TCACACTAAC	660
TTTGAAGGTG AAGTTTACGT TCTTTCCAAA GAGGAAGGCG GACGACACAC TCCATTCTTC	720
AATGGATACC GACCTCAGTT CTATGTTAGA ACTACAGACG TTACCGGTTT TATCTCTCTT	780
CCTGAGGGCG TAGAGATGGT TATGCCTGGT GACAACGTTA AGATCAATGT TGAGCTTATC	840
GCTCCTGTAG CCCTCGAAGA GGGAACACGA TTCGCGATCC GTGAAGGTGG TCGAACCGTT	900
GGTGCGGGT	909

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:18
- (D) OTHER INFORMATION:/note= "n = inosine"

- 155 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

TARTCNGTRA ANGCYTCNAC RCACAT

26

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

TCTTTAGCAG AACAGGATGA A

21

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

GAATAATTCC ATATCCTCCG

20

CLAIMS**What is claimed is:**

1. A method using probes and/or amplification primers which are specific, ubiquitous and sensitive for determining the presence and/or amount of nucleic acids:
 - 5 - from a bacterial antibiotic resistance gene selected from the group consisting of *bla_{tem}*, *bla_{shv}*, *bla_{rob}*, *bla_{oxa}*, *bla_Z*, *aadB*, *aacC1*, *aacC2*, *aacC3*, *aac6'-IIa*, *aacA4*, *aad(6')*, *vanA*, *vanB*, *vanC*, *msrA*, *satA*, *aac(6')-aph(2'')*, *vat*, *vga*, *ermA*, *ermB*, *ermC*, *mecA*, *int* and *sul*, and
 - from specific bacterial and fungal species selected from the group consisting
 - 10 of *Enterococcus faecium*, *Listeria monocytogenes*, *Neisseria meningitidis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae*, *Candida albicans*, *Enterococcus* species, *Neisseria* species, *Staphylococcus* species, *Streptococcus* species and *Candida* species,
- in any sample suspected of containing said bacterial and/or fungal nucleic acids,
- 15 wherein each of said nucleic acid or variant or part thereof comprises a selected target region hybridizable with said probes or primers;
 - said method comprising the following steps: contacting said sample with said probes or primers and detecting the presence and/or amount of hybridized probes or amplified products as an indication of the presence and/or amount of said specific
 - 20 bacterial and/or fungal species and bacterial antibiotic resistance genes.
2. A method according to claim 1, which further makes use of probes and/or primers which are specific, ubiquitous and sensitive for determining the presence and/or amount of nucleic acids from any bacterium or fungus.
3. The method of claim 1, which is performed directly from a test sample.
- 25 4. The method of claim 1, which is performed directly from a test sample consisting of a bacterial and/or fungal culture or suspension.
5. The method of claim 1, wherein said nucleic acids are all detected under uniform hybridization or amplification conditions.
6. The method of claim 1, wherein said nucleic acids are amplified by a method
 - 30 selected from the group consisting of:
 - a) polymerase chain reaction (PCR),
 - b) ligase chain reaction (LCR),
 - c) nucleic acid sequence-based amplification (NASBA),

- d) self-sustained sequence replication (3SR),
- e) strand displacement amplification (SDA),
- f) branched DNA signal amplification (bDNA),
- g) transcription-mediated amplification (TMA),
- 5 h) cycling probe technology (CPT),
- i) nested PCR, and
- j) multiplex PCR.

7. The method of claim 6, wherein said nucleic acids are amplified by PCR.

10 8. The method of claim 7, wherein the PCR protocol achieves within one hour under uniform amplification conditions the determination of the presence of said nucleic acids by performing for each amplification cycle an annealing step of thirty seconds at 45-55°C and a denaturation step of only one second at 95°C without any time specifically allowed to an elongation step.

15 9. A method for the detection, identification and/or quantification of a microorganism selected from the group consisting of *Enterococcus faecium*, *Listeria monocytogenes*, *Neisseria meningitidis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae*, *Candida albicans*, *Enterococcus* species, *Neisseria* species, *Staphylococcus* species, *Streptococcus* species and *Candida* species, directly from a test sample or from bacterial and/or fungal cultures, which comprises the following steps:

20

a) depositing and fixing on an inert support or leaving in solution the said microorganism DNA of the sample or of a substantially homogeneous population of said microorganism isolated from this sample, or

25 inoculating said sample or said substantially homogeneous population of microorganism isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or said isolated microorganism to release the said microorganism DNA,

said microorganism DNA being made in a substantially single-stranded form;

30 b) contacting said single-stranded DNA with a probe, said probe comprising at least one single-stranded nucleic acid which nucleotide sequence is selected from the group consisting of SEQ ID NOs: 26, 27, 28, 29, 30, 120, 131 to 134, 31, 140 to 143, 32 to 36, 120 to 124, a sequence complementary thereof, a part thereof having at least 12 nucleotides in length, and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Enterococcus faecium*, *Listeria*

5 *monocytogenes*, *Neisseria meningitidis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae*, *Candida albicans*, *Enterococcus* species, *Neisseria* species, *Staphylococcus* species, *Streptococcus* species and *Candida* species, respectively, under conditions such that the nucleic acid of said probe can selectively hybridize with said microorganism DNA, whereby a hybridization complex is formed; and

c) detecting the presence of said hybridization complex on said inert support or in said solution as an indication of the presence and/or amount of said microorganism, in said test sample.

10 10. A method for detecting the presence and/or amount of a microorganism selected from the group consisting of *Enterococcus faecium*, *Listeria monocytogenes*, *Neisseria meningitidis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae*, *Candida albicans*, *Enterococcus* species, *Neisseria* species, *Staphylococcus* species, *Streptococcus* species and *Candida* species, in a test sample which comprises the following steps:

15 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said microorganism DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an
20 extension product which contains the target sequence as a template, said at least one pair of primers being chosen from a nucleotide sequence within the group consisting of SEQ ID NOs: 26, 27, 28, 29, 30, 120, 131 to 134, 31, 140 to 143, 32 to 36, 120 to 124, respectively with regard to said microorganism, a sequence complementary thereof, and a variant thereof;

25 b) synthesizing an extension product of each of said primers, said extension product containing the target sequence, and amplifying said target sequence, if any, to a detectable level; and

30 c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of said microorganisms, in said test sample.

35 11. The method of claim 10, wherein said pair of primers is defined in SEQ ID NOs: 1 and 2, 3 and 4, 5 and 6, 7 and 8, 9 and 10, 11 and 12, 13 and 14, 15 and 16, 17 to 20, 21 and 22, respectively, for each of *Enterococcus faecium*, *Listeria monocytogenes*, *Neisseria meningitidis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae*, *Candida albicans*, *Enterococcus* species, *Neisseria* species, *Staphylococcus* species and *Streptococcus* species.

12. A method for detecting the presence and/or amount of any bacterium directly from a test sample or a bacterial culture, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogeneous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogeneous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being made in a substantially single-stranded form;

b) contacting said single-stranded DNA with a probe, said probe comprising at least one single-stranded nucleic acid which nucleotide sequence is selected from the group consisting of SEQ ID NOs: 118, 119, 125 to 171, a sequence complementary thereof, a part thereof having at least 12 nucleotides in length, and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of any bacterial species, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed; and

c) detecting the presence of said hybridization complex on said inert support or in said solution as an indication of the presence and/or amount of any bacterium in said test sample.

13. A method for detecting the presence and/or amount of any bacterium in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of any bacterial DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from a nucleotide sequence within the group consisting of SEQ ID NO: 118, 119, 125 to 171, a sequence complementary thereof, and a variant thereof;

b) synthesizing an extension product of each of said primers, said extension product containing the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of any bacterium in said test sample.

14. The method of claim 13, wherein said pair of primers is defined in SEQ ID NOs: 23 and 24.

15. A method for obtaining *tuf* sequences from any bacterium directly from a test sample or a bacterial culture, which comprises the following steps:

5 a) treating said sample with an aqueous solution containing a pair of primers having a sequence selected within the nucleotide sequences defined in SEQ ID NOs: 107 and 108, a part thereof having at least 12 nucleotides in length, a sequence complementary thereof, and a variant thereof, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial *tuf*
10 gene that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template;

b) synthesizing an extension product of each of said primers, said extension product containing the target sequence, and amplifying said target sequence, if any,
15 to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence; and

d) determining the nucleotide sequence of the said amplified target sequence by using any DNA sequencing method.

16. A method for detecting the presence and/or amount of any fungus directly from
20 a test sample or a fungal culture, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the fungal DNA of the sample or of a substantially homogeneous population of fungi isolated from this sample, or

inoculating said sample or said substantially homogeneous population of fungi
25 isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated fungi to release the fungal DNA,

said fungal DNA being made in a substantially single-stranded form;

b) contacting said single-stranded DNA with a probe, said probe comprising at least one single-stranded nucleotide sequence selected from the group consisting of
30 SEQ ID NOs: 120 to 124, a sequence complementary thereof, a part thereof having at least 12 nucleotides in length, and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of any fungus, under conditions such that the nucleic acid of said probe can selectively hybridize with said fungal DNA, whereby a hybridization complex is formed; and

35 c) detecting the presence of said hybridization complex on said inert support or

in said solution as an indication of the presence and/or amount of any fungus in said test sample.

17. A method for detecting the presence and/or amount of any fungus in a test sample which comprises the following steps:

5 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of any fungal DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product
10 which contains the target sequence as a template, said at least one pair of primers being chosen from a nucleotide sequence within the group consisting of SEQ ID NOs: 120 to 124, a sequence complementary thereof, and a variant thereof;

 b) synthesizing an extension product of each of said primers, said extension product containing the target sequence, and amplifying said target sequence, if any,
15 to a detectable level; and

 c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of any fungus in said test sample.

18. A method for obtaining *tuf* sequences from any fungus directly from a test sample or a fungal culture, which comprises the following steps:

20 a) treating said sample with an aqueous solution containing a pair of primers having a sequence selected within the nucleotide sequence defined in SEQ ID NOs: 109 and 172, a part thereof having at least 12 nucleotides in length, a sequence complementary thereof, and a variant thereof, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said fungal *tuf*
25 gene that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template;

 b) synthesizing an extension product of each of said primers, said extension product containing the target sequence, and amplifying said target sequence, if any,
30 to a detectable level; and

 c) detecting the presence and/or amount of said amplified target sequence; and

 d) determining the nucleotide sequence of the said amplified target sequence by using any DNA sequencing method.

19. A method as defined in claim 1, which comprises the evaluation of the presence
35 of a bacterial resistance mediated by a bacterial antibiotic resistance gene selected

from the group consisting of *bla_{oxa}*, *blaZ*, *aac6'-IIa*, *ermA*, *ermB*, *ermC*, *vanB*, *vanC*, directly from a test sample or a bacterial culture, which comprises the following steps:

5 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogeneous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogeneous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being made in a substantially single-stranded form;

10 b) contacting said single-stranded DNA with a probe, said probe comprising at least one single-stranded nucleotide sequence having at least 12 nucleotide in length is selected from the group consisting of SEQ ID NOs: 110, 111, 112, 113, 114 115, 116, 117, a sequence complementary thereof, and a variant thereof, which specifically hybridizes with said bacterial antibiotic resistance gene, respectively; and

15 c) detecting the presence of a hybridization complex as an indication of a bacterial resistance mediated by said one of said bacterial antibiotic resistance genes.

20. A method as defined in claim 1, which comprises the evaluation of the presence of a bacterial resistance mediated by a bacterial antibiotic resistance gene selected from the group consisting of *bla_{oxa}*, *blaZ*, *aac6'-IIa*, *ermA*, *ermB*, *ermC*, *vanB*, *vanC*,
20 directly from a test sample or a bacterial culture, which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene that contains a target sequence, and the other of said
25 primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from a nucleotide sequence within the group consisting of SEQ ID NOs: 110, 111, 112, 113, 114, 115, 116, 117, respectively with regard to said bacterial antibiotic resistance gene, a sequence complementary thereof, and a
30 variant thereof;

b) synthesizing an extension product of each of said primers, said extension product containing the target sequence, and amplifying said target sequence, if any, to a detectable level; and

35 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance mediated by one of said bacterial antibiotic resistance genes.

21. A method as defined in claim 1, which comprises the evaluation of the presence of a bacterial resistance gene selected from the group consisting of *bla_{tem}*, *bla_{shv}*, *bla_{rob}*, *bla_{oxa}*, *bla_Z*, *aadB*, *aacC1*, *aacC2*, *aacC3*, *aac6'-IIa*, *aacA4*, *aad(6')*, *vanA*, *vanB*, *vanC*, *msrA*, *satA*, *aac(6')-aph(2'')*, *vat*, *vga*, *ermA*, *ermB*, *ermC*, *mecA*, *int* and *sul*, directly from a test sample or a bacterial culture, which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of primers having a sequence selected in the group consisting of SEQ ID NOs: 37 to 40, 41 to 44, 45 to 48, 49 and 50, 51 and 52, 53 and 54, 55 and 56, 57 and 58, 59 to 60, 61 to 64, 65 and 66, 173 and 174, 67 to 70, 71 to 74, 75 and 76, 77 to 80, 81 and 82, 83 to 86, 87 and 88, 89 and 90, 91 and 92, 93 and 94, 95 and 96, 97 and 98, 99 to 102, 103 to 106, a part thereof having at least 12 nucleotides in length, a sequence complementary thereof, a variant thereof, and mixtures thereof, one of said primers of said pair being capable of hybridizing selectively with one of the two complementary strands of its respective bacterial antibiotic resistance gene that contains a target sequence, and the other of said primers of said pairs being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template;

b) synthesizing an extension product of each of said primers, said extension product containing the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance mediated by one of said bacterial antibiotic resistance genes.

22. A nucleic acid having the nucleotide sequence of any one of SEQ ID NOs: 26 to 36, 110 to 171, a part thereof, a sequence complementary thereof, and variant thereof which, when in single-stranded form, ubiquitously and specifically hybridizes with a target bacterial or fungal DNA as a probe or as a primer.

23. An oligonucleotide having the nucleotide sequence of any one of SEQ ID NOs: 1 to 25, 37 to 109, 172 to 174, a part thereof, a sequence complementary thereof, and variant thereof, which ubiquitously and specifically hybridizes with a target bacterial or fungal DNA as a probe or as a primer.

24. A recombinant plasmid comprising a nucleic acid as defined in claim 22.

25. A recombinant host which has been transformed by a recombinant plasmid according to claim 24.

26. A recombinant host according to claim 25 wherein said host is *Escherichia coli*.

27. A diagnostic kit for the detection and/or quantification of the nucleic acids of any

combination of the microbial species and/or genera selected from the group consisting of *Enterococcus faecium*, *Listeria monocytogenes*, *Neisseria meningitidis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae*, *Candida albicans*, *Enterococcus* species, *Neisseria* species, *Staphylococcus* species, *Streptococcus* species and *Candida* species, comprising any suitable combination of probes of at least 12 nucleotides in length selected from the group consisting of SEQ ID NOs: 26 to 36, 120 to 124, 131 to 134, 140 to 143, sequences complementary thereof, and variants thereof.

28. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the microbial species and/or genera selected from the group consisting of *Enterococcus faecium*, *Listeria monocytogenes*, *Neisseria meningitidis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae*, *Candida albicans*, *Enterococcus* species, *Neisseria* species, *Staphylococcus* species, *Streptococcus* species and *Candida* species, comprising any suitable combination of primers of at least 12 nucleotides in length selected from the group consisting of SEQ ID NOs: 26 to 36, 120 to 124, 131 to 134, 140 to 143, sequences complementary thereof, and variants thereof.

29. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the microbial species and/or genera selected from the group consisting of *Enterococcus faecium*, *Listeria monocytogenes*, *Neisseria meningitidis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae*, *Candida albicans*, *Enterococcus* species, *Neisseria* species, *Staphylococcus* species and *Streptococcus* species, comprising any suitable combination of primers selected from the group consisting of SEQ ID NOs: 1 to 22, parts thereof having at least 12 nucleotides in length, sequences complementary thereof, and variants thereof.

30. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial resistance genes selected from the group consisting of *bla_{oxa}*, *blaZ*, *aac6'-IIa*, *ermA*, *ermB*, *ermC*, *vanB*, *vanC*, comprising any suitable combination of probes of at least 12 nucleotides in length selected from the group consisting of SEQ ID NOs: 110 to 117, sequences complementary thereof, and variants thereof.

31. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial resistance genes selected from the group consisting of *bla_{oxa}*, *blaZ*, *aac6'-IIa*, *ermA*, *ermB*, *ermC*, *vanB*, *vanC*, comprising any suitable combination of primers of at least 12 nucleotides in length selected from the group consisting of SEQ ID NOs: 110 to 117, sequences complementary thereof, and variants thereof.

32. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial resistance genes selected from the group consisting of *bla_{tem}*, *bla_{shv}*, *bla_{rob}*, *bla_{oxa}*, *blaZ*, *aadB*, *aacC1*, *aacC2*, *aacC3*, *aac6'-IIa*, *aacA4*, *aad(6')*, *vanA*, *vanB*, *vanC*, *msrA*, *satA*, *aac(6')-aph(2'')*, *vat*, *vga*, *ermA*, *ermB*, *ermC*, *mecA*, *int* and *sul*, comprising any suitable combination of primers selected from the group consisting of SEQ ID NOs: 37 to 106, 173 and 174, a part thereof having at least 12 nucleotides in length, sequences complementary thereof, and variants thereof.
- A diagnostic kit for the detection and/or quantification of the nucleic acids of any bacterium and/or fungus, comprising any combination of probes of at least 12 nucleotides in length selected from the group consisting of SEQ ID NOs: 118 to 171, sequences complementary thereof, and variants thereof.
34. A diagnostic kit for the detection and/or quantification of the nucleic acids of any bacterium and/or fungus, comprising any suitable combination of primers of at least 12 nucleotides in length selected from the group consisting of SEQ ID NOs: 118 to 171, sequences complementary thereof, and variants thereof.
35. A diagnostic kit for the detection and/or quantification of the nucleic acids of any bacterium, comprising a pair of primers having a sequence selected within the nucleotide sequence defined in SEQ ID NOs: 23 and 24, parts thereof having at least 12 nucleotides in length, sequences complementary thereof, and variants thereof.
36. A diagnostic kit, as defined in claim 27, further comprising any combination of probes of at least 12 nucleotides in length selected within a nucleotide sequence from the group consisting of SEQ ID NOs: 118 to 171, sequences complementary thereof, and variants thereof, for the simultaneous detection and/or quantification of nucleic acids of any bacterium and/or fungus.
37. A diagnostic kit, as defined in claim 28, further comprising any suitable combination of primers of at least 12 nucleotides in length selected within a nucleotide sequence from the group consisting of SEQ ID NOs: 118 to 171, sequences complementary thereof, and variants thereof, for the simultaneous detection and/or quantification of nucleic acids of any bacterium and/or fungus.
38. A diagnostic kit, as defined in claim 29, further comprising a pair of primers having a sequence selected within the nucleotide sequence defined in SEQ ID NOs: 23 and 24, parts thereof having at least 12 nucleotides in length, sequences complementary thereof, and variants thereof, for the simultaneous detection and/or quantification of nucleic acids of any bacterium.
39. A diagnostic kit, as defined in claim 27, further comprising any combination of probes of at least 12 nucleotides in length selected within a nucleotide sequence from

the group consisting of SEQ ID NOs: 110 to 117, sequences complementary thereof, and variants thereof, for the simultaneous detection and/or quantification of nucleic acids of any bacterial antibiotic resistance gene selected from the group consisting of *bla_{oxa}*, *blaZ*, *aac6'-IIa*, *ermA*, *ermB*, *ermC*, *vanB*, *vanC*.

- 5 40. A diagnostic kit, as defined in claim 28, further comprising any suitable combination of primers of at least 12 nucleotides in length selected within a nucleotide sequence from the group consisting of SEQ ID NOs: 110 to 117, sequences complementary thereof, and variants thereof, for the simultaneous detection and/or quantification of nucleic acids of any bacterial antibiotic resistance gene selected from the group consisting of *bla_{oxa}*, *blaZ*, *aac6'-IIa*, *ermA*, *ermB*, *ermC*, *vanB*, *vanC*.

- 10 41. A diagnostic kit, as defined in claim 29, further comprising any suitable combination of primers of at least 12 nucleotides in length selected within a nucleotide sequence from the group consisting of SEQ ID NOs: 37 to 106, 173 and 174, sequences complementary thereof, and variants thereof, for the simultaneous detection and/or quantification of nucleic acids of any bacterial antibiotic resistance gene selected from the group consisting of *bla_{tem}*, *bla_{rob}*, *bla_{shv}*, *bla_{oxa}*, *blaZ*, *aadB*, *aacC1*, *aacC2*, *aacC3*, *aacA4*, *aac6'-IIa*, *aad(6')*, *ermA*, *ermB*, *ermC*, *mecA*, *vanA*, *vanB*, *vanC*, *satA*, *aac(6')-aph(2'')*, *vat*, *vga*, *msrA*, *sul* and *int*.

- 15 42. A diagnostic kit, as defined in claim 30, further comprising any combination of probes of at least 12 nucleotides in length selected within a nucleotide sequence from the group consisting of SEQ ID NOs: 118 to 171, sequences complementary thereof, and variants thereof, for the simultaneous detection and/or quantification of nucleic acids of any bacterium and/or fungus.

- 20 43. A diagnostic kit, as defined in claim 31, further comprising any suitable combination of primers of at least 12 nucleotides in length selected within a nucleotide sequence from the group consisting of SEQ ID NOs: 118 to 171, sequences complementary thereof, and variants thereof, for the simultaneous detection and/or quantification of nucleic acids of any bacterium and/or fungus.

- 25 44. A diagnostic kit, as defined in claim 32, further comprising a pair of primers having a sequence selected within the nucleotide sequence defined in SEQ ID NOs: 23 and 24, parts thereof having at least 12 nucleotides in length, sequences complementary thereof, and variants thereof, for the simultaneous detection and/or quantification of nucleic acids of any bacterium.

- 30 45. A diagnostic kit, as defined in claim 39, further comprising any combination of probes of at least 12 nucleotides in length selected within a nucleotide sequence from the group consisting of SEQ ID NOs: 118 to 171, sequences complementary thereof, and variants thereof, for the simultaneous detection and/or quantification of nucleic acids of any bacterium and/or fungus.

acids of any bacterium and/or fungus.

- 5 46. A diagnostic kit, as defined in claim 40, further comprising any suitable combination of primers of at least 12 nucleotides in length selected within a nucleotide sequence from the group consisting of SEQ ID NOs: 118 to 171, sequences complementary thereof, and variants thereof, for the simultaneous detection and/or quantification of nucleic acids of any bacterium and/or fungus.

- 10 47. A diagnostic kit, as defined in claim 41, further comprising a pair of primers having a sequence selected within the nucleotide sequence defined in SEQ ID NOs: 23 and 24, parts thereof having at least 12 nucleotides in length, sequences complementary thereof, and variants thereof, for the simultaneous detection and/or quantification of nucleic acids of any bacterium.